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Database
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Maximum DB
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Perfect score:
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iter than or equal to the score of the result being printed,
cived by analysis of the total score distribution.
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Gapop 60.0 , Gapext 60.0
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Copyright (c) 1993 - 2000 Comp
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	Dumas Milne Edwards J. Duclert A. Giordano J:	(GEGT) GENOET.	(CECH) CENCER	26-FEB-1999; 99US-0122487.		21-FEB-2000; 2000EP-0200610.		06-SEP-2000.		EP1033401-A2.		Homo sapiens.		SS	Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation:		Human secreted protein 5' EST, SEO ID NO: 27258.		06-OCT-2000 (first entry)		AAC23183;		AAC23183 standard; cDNA; 82 BP.	AAC23183/c	JLT 1

PT PT XX

WPI; 2000-500381/45.

Claim 1; SEQ ID 27258; 71pp + CD-ROM; English.

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

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AAC23260/c
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Best Local
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        The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included.
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                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
                                                                                                                                                                                Claim 1; SEQ ID 27335; 71pp + CD-ROM; English.
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sequences have been STs are derived from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expressed sequence tag; secreted protein; cDNA isolation; chromosome mapping; ss.
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mRNAs with intact 5' ends
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                                                                                                                                                                                                               mapping procedures
and can
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RESULT 3
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Best Local
                                  of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                 total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from all mainly to the 3' untranslated region (UTR)
                                                                                                                                                                                                                      The present sequence is one of a large number of 5' ESTs derived
                                                                                                                                                                                                                                                         Claim 1; SEQ ID 22489;
                                                                                                                                                                                                                                                                                                New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and fo
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                                                                                                                                                                                           identified within the present sequence.
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                                                                                                                                                                                           encoding secreted proteins. No ORF has yet been conclusively ified within the present sequence. The 5' ESTs were prepared
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larity 100.0%;
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mapping; ss.
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Pred. No. 0.15;
Mismatches
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Query Match
Best Local Similarity
Matches 18; Conserv

Conservative

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Mismatches

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0.15; DB 21;

Length 126;

100.0%; Score 18; 100.0%; Pred. No.

Sequence 126 BP;

23 A; 49 C;

30 G;

24 T; 0 other

and secretion

vectors

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RESULT 5
AAC04894/c
ID AAC04894 standard; cDNA; 134
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                                                                                            В
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ID AAC284
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                                                                                                                                                  Matches
                                                                                                                                                                Best
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                 of the mRNA because they are often obtained from oligo-dy primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                             The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                  Sequence 131 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 32567; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAC28492 standard; cDNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC28492;
                                                                                            56
                                                                                                                                                             Local
                                                                                                                 1 ggcggagcttgcagtgag 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50
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                                                                                                                                                 l Similarity
18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5' EST;
                                                                                                                                                                                                                                             and secretion
                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein 5'
                                                                                                                                                                                                               22 A; 46 C; 35 G; 28
                                                                                                                                                            100.0%;
                                                                                           39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Duclert A,
                                                                                                                                                                                                                                            vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  131 BP
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                                                                                                                                              0
                        ₽P.
                                                                                                                                                             Pred. No.
                                                                                                                                                                         Score 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO: 32567
                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Giordano J;
                                                                                                                                                                                                                 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 secreted protein; cDNA isolation;
                                                                                                                                                          0.15;
                                                                                                                                                                                                                 0 other
                                                                                                                                                                      DB 21;
                                                                                                                                              <u>.</u>
                                                                                                                                                                      Length 131;
                                                                                                                                              Indels
                                                                                                                                           0;
                                                                                                                                           Gaps
                                                                                                                                           0;
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AAC04894;

EP1033401-A2

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RESULT 6
AAC18209/c
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                                                                                                                                                                                                                                                             QΥ
                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                         Matches
                       Homo sapiens
                                                gene therapy;
                                                                                                                                                                   AAC18209 standard; cDNA; 135
                                                                                                                                                                                                                                                                                                                                                       Sequence 134 BP; 18 A; 49 C;
                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                Human;
                                                                                         Human secreted
                                                                                                                   06-OCT-2000
                                                                                                                                             AAC18209;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                  expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID 8969; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnostic, forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-OCT-2000 (first entry)
                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2000-500381/45
                                                      5' EST; expressed sequence tag; secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5' EST; expressed sequence tag; secreted protein; cDNA isolation;
herapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                (first entry)
                                              chromosome mapping;
                                                                                       protein 5' EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9908-0122487
                                                                                                                                                                                                                                                                                                   100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                      43
                                                                                                                                                                                                                                                             18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                 vectors.
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                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                        35
                                                                                                                                                                                                                                                                                                    Score 18;
Pred. No.
                                                                                      SEQ ID NO: 22284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                        <u>ი</u>
                                                                                                                                                                                                                                                                                        Mismatches
                                                 SS
                                                                                                                                                                                                                                                                                                                                                        28 T; 4 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Giordano
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                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                               Length 134;
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                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                     Gaps
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Best I
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                                                                                                                                                                                                                                                                                                                                                11987/с
                                                                                                                                                                                                   Human; 5' EST; expressed sequence tag;
gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA, because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion upstream
           Dumas Milne Edwards
                                                               26-FEB-1999;
                                                                                         21-FEB-2000; 2000EP-0200610
                                                                                                                      06-SEP-2000
                                                                                                                                                 EP1033401-A2
                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                                                             Human secreted protein 5' EST, SEQ ID NO: 16062
                                                                                                                                                                                                                                                                           06-OCT-2000
                                                                                                                                                                                                                                                                                                      AAC11987
                                                                                                                                                                                                                                                                                                                                AAC11987 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        expression and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID 22284; 71pp + CD-ROM; English.
                                     (GEST ) GENSET.
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                                                                                                                                                                                                                                                                                                                                                                                                      107
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity hes 18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                1 ggcggagcttgcagtgag 18
                                                                                                                                                                                                                                                                                                                                                                                                    GGCGGAGCTTGCAGTGAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            135 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                       (first entry)
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                                                                 99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27
                                                                                                                                                                                                                                                                                                                                cDNA; 138
          Ç
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         35 C;
          Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                    90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                ВP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           G; 44 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Giordano
       Giordano J;
                                                                                                                                                                                                              secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0.15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21; Length 135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       o,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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SXCCCCCCCCCCCX PX P P P X R
                                                                total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends of therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion upstream regulatory sequences and to design
     Sequence 138
                                                                                                                                                                                                                                                                                                                         The present sequence is one of a large number of 5' EmmRNAs encoding secreted proteins. No ORF has yet been identified within the present sequence. The 5' ESTs we
                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID 16062; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New nucleic acid that is a 5' expressed sequence tag (5' EST) obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and
                                                      expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-500381/45
     BP;
     21
  A; 47 C;
  34 G;
35 T; 1 other;
                                                                                                                                                                                                                                                                                                                         ESTs were prepared from
                                                                                                                                                                                                                                                                                                                                                                          ESTs derived
                                                                                                                                                                                                                                                                                                                                                     conclusively
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and
                                                                                                                                                                                                                                                                                                                                                                          from
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Matches
75 GGCGGAGCTTGCAGTGAG 58
                                       Local
        1 ggcggagcttgcagtgag
                                18;
                                       Similarity
                                Conservative
                                      100.0%;
               18
                                0
                                      Score 18; DB 2
Pred. No. 0.15;
                               Mismatches
                                              21;
                               0,
                                            Length 138;
                              Indels
                              0
                             Gaps
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RESULT 8
AAC15609/c
AC15609 standard; cDNA; 138
21-FEB-2000; 2000EP-0200610
                            06-SEP-2000.
                                                       EP1033401-A2
                                                                                 Homo sapiens
                                                                                                          gene therapy;
                                                                                                                            Human; 5' EST;
                                                                                                                                                                               06-OCT-2000
                                                                                                                                                    Human secreted
                                                                                                                                                                                                          AAC15609
                                                                                                                                                                             (first entry)
                                                                                                         ; expressed sequence tag;
chromosome mapping; ss.
                                                                                                                                                    protein 5'
                                                                                                                                                    EST,
                                                                                                                                                                                                                                    ВP
                                                                                                                                                    SEQ ID
                                                                                                                                                    NO: 19684.
                                                                                                                    secreted protein; cDNA isolation;
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CCCCXXX

(GEST) GENSET 26-FEB-1999;

99US-0122487

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from

ESTs were prepared from

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures

WPI; 2000-500381/45. Dumas Milne Edwards J,

Duclert A,

Giordano J;

Claim 1; SEQ

ID 19684; 71pp + CD-ROM; English.

999999999988%&

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Query Match
Best Local S
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mRNAs encoding secreted proteins. No OFF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                 New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond diagnostic, forensic, gene therapy and chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                            The present sequence is one of a large number of 5' ESTs derived
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-500381/45
                                                                                                                                                                                                                                                                                                                                                    Claim
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 138 BP; 36 A; 36 C; 36 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGCGGAGCTTGCAGTGAG 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     therapy;
                                                                                                                                                                                                                                                                                                                                                    ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Milne Edwards J,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                    SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and secretion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                    IJ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expressed
                                                                                                                                                                                                                                                                                                                                               19765;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                                                                                                                                                                                                                                          71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  mapping;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence tag; secreted protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EST,
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Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO: 19765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18;
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T; 0
                                                                                                                                                                                                                                                                                                                                                                                           chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 .15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21;
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                                                                                                                                                                                                                                                                                                                                                                                                            tag (5' EST) for to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 138;
                                                                                                                                                                                                                                                                                                                                                                                    mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                      procedures
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Query Match Best Local S Matches 18

l Similarity 18; Conserv

Conservative

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Mismatches

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Gaps

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100.0%;

Score 18; DB 2: Pred. No. 0.14;

DB 21;

Length 167;

Sequence 167

BP;

21 A; 58 C;

35 G;

48

T; 5 other;

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RESULT 10
AAC05392/c
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Matches 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                     mRNAs encoding secreted proteins. No OFF has yet been conclusively identified within the present sequence. The 5' ESTS were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA ilbraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                  The present sequence is one of a large number of 5' ESTs derived mRNAs encoding secreted proteins. No ORF has yet been conclusivel
                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                  diagnostic,
                                                                                                                                                                                                                                                            New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
                                                                                                                                                                                                                                                                                                                                Dumas Milne Edwards
                                                                                                                                                                                                                                                                                                                                                                                                            21-FEB-2000; 2000EP-0200610
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gene therapy;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-OCT-2000
                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                      26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EP1033401-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAC05392;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     83 ggcggagcttgcagtgag 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 ggcggagcttgcagtgag
                                                                                                                                                                                                                                                                                                        2000-500381/45.
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                                                                                                                                                                                                                        SEQ ID 9467;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EST;
                                                                                                                                                                                                                                                  forensic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome mapping;
                                                                                                                                                                                                                                                                                                                                                                                    99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              expressed sequence tag;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein 5' EST,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA;
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                                                                                                                                                                                                                     71pp + CD-ROM; English.
                                                                                                                                                                                                                                                  gene
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                                                                                                                                                                                                                                                                                                                               Duclert A,
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                                                                                                                                                                                                                                           therapy and
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQ ID NO: 9467.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SS.
                                                                                                                                                                                                                                                                                                                              Giordano
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Τ,
                                                                                                                                                                                                                                             chromosome mapping procedures
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein; cDNA isolation;
                                                                                                                                                                                                                                                            tag (5' EST) for to 5'ESTs and fo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 151;
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AAC04655/c
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AAC11951
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                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore because the second of the se
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Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 172 BP; 51 A; 45 C; 53 G; 23 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; SEQ ID 16026; 71pp + CD-ROM; English.
                                                   06-OCT-2000
                                                                                                  AAC04655;
                                                                                                                                              AAC04655 standard; cDNA; 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-500381/45.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human; '5' EST; expressed sequence tag; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GEST ) GENSET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                26-FEB-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-OCT-2000
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                                                                                                                                                                                                                                                                  87 ggcggagcttgcagtgag 104
                                                                                                                                                                                                                                                                                                                                                                          Local Similarity hes 18; Conserv
                                                                                                                                                                                                                                                                                               1 ggcggagcttgcagtgag 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                    100.0%; ilarity 100.0%; Conservative
                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein 5' EST,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172
EST,
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                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 2:
Pred. No. 0.14;
SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO: 16026
                                                                                                                                                                                                                                                                                                                                                                          Mismatches
ID NO: 8730
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Giordano J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     secreted protein; cDNA isolation;
                                                                                                                                                                                                                                                                                                                                                                                                                   DB 21;
                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                Length 172;
                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                    0,
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Query Match
Best Local S
Matches 18
                                                                                                                                        Sequence 182 BP; 22 A; 46 C; 35 G; 78 T; 1 other;
                                                                                                                                                                                                                       libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design
                                                                                                                                                                                                                                                                                                                                                                                                                 The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-dT primed cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
                                                                                                                                                                                                  expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; SEQ ID 8730; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
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        Local Similarity
nes 18; Conserv
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  100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   chromosome mapping; ss.
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        0,
                                  Score 18;
Pred. No.
     Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; cDNA isolation;
                               0.14;
                                                       DB 21;
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  0;
                                                       Length 182;
  Indels
  0
Gaps
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PR

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18
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AAC16191
                           RESULT
AAC16191;
             AAC16191 standard; cDNA; 185 BP
                                                13
                                                .157
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В Qγ

06-SEP-2000 Human; 5' EST;
gene therapy; (EP1033401-A2 Homo sapiens ; expressed chromosome sequence tag; secreted protein; cDNA isolation; mapping; ss.

21-FEB-2000; 2000EP-0200610.

X PX A

06-OCT-2000

(first entry)

Human secreted protein 5' EST,

SEQ ID NO: 20266

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PPT XXX
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Best Local S
Matches 18
                                WPI; 2000-500381/45
                                                        Dumas Milne Edwards
                                                                                                                               21-FEB-2000; 2000EP-0200610
                                                                                                                                                                                                                                                                                         06-OCT-2000
                                                                                                                                                                                                                                                                                                                                        AAC22610 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               of the mRNA because they are often obtained from oligo-dT prined cDNA libraries. Such ESTs are not well suited for isolating cDNA sequences derived from the 5' ends of mRNAs and even in those cases where longer cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
                                                                                                         26-FEB-1999;
                                                                                                                                                        06-SEP-2000
                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                               gene
                                                                                                                                                                                                                                           Human;
                                                                                                                                                                                                                                                                Human secreted protein 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 185 BP; 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is one of a large number of 5' ESTs derived mRNAs encoding secreted proteins. No ORF has yet been conclusivel identified within the present sequence. The 5' ESTs were prepared total human RNAs or polyA+ RNAs derived from 30 different tissues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New nucleic acid that is a 5' expressed sequence obtaining cDNAs and genomic DNAs that correspond
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                                                                                                                                                                                                                             therapy;
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                                                                                                                                                                                                                          expressed sequence chromosome mapping;
                                                                                                        99US-0122487
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                                                        Duclert
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                                                                                                                                                                                                                                                                                                                                        ВP
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                                                                                                                                                                                                                                                               SEQ ID NO: 26685
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                                                                                                                                                                                                                                       tag;
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                                                        Giordano
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                                                                                                                                                                                                                                      protein;
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New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for

The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORF has yet been conclusively identified within the present sequence. The 5' ESTs were prepared from total human RNAs or polyA+ RNAs derived from 30 different tissues. ESTs sequences usually correspond mainly to the 3' untranslated region (UTI) of the many boosties the many boosties.

ESTs were prepared from

(UTR) EST

are often obtained from oligo-dT not well suited for isolating cD

New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedure

procedures

Claim

1; SEQ

ID 26546;

71pp + CD-ROM; English.

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cc identified within the present sequence. The 5' ESTs derived from cc total human RNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) cof the mRNA because they are often obtained from oligo-dT primed cDNA cc libraries. Such ESTs are not well suited for isolating cDNA sequences cc derived from the 5' ends of mRNAs and even in those cases where longer cc cDNA sequences have been obtained, the full 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5' ends and can therefore be cc used to obtain full length cDNAs and genomic DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design of the pression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 15
AAC22471/c
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Best Local S
Matches 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                          AAC22471;
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20-JUN-1997;
22-JUL-1997;
22-JUL-1997;
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New isolated Borrelia burgdorferi nucleic acids
                        WPI; 1999-189980/16
P-PSDB; AAY19875.
                                                                                                                                                                                                                                                                      B. burgdorferi antigenic protein coding sequence, t617.nt
                                                                                                                                                                                       30-DEC-1998
                                                                                                                                                                                                          WO9859071-A1.
                                                                                                                                                                                                                                                Antigenic protein; vaccine; Lyme disease; infection; detection; ss
                                                                            (HUMA-) HUMAN GENOME SCI INC (MEDI-) MEDIMMUNE INC.
                                                                                                                                                                                                                              Borrelia burgdorferi.
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                                                       Erwin AL,
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97US-0050359.
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                                                      Lathigra
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used to develop
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Human secreted pro
Human PPAR-gamma-2
Thermophilic bacte
C. elegans SPE-4 D
Colon cancer assoc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human breast cance
Human breast cance
Human secreted pro
Human secreted pro
DNA encoding the C
PRLTS coding seque
PDGF receptor beta
Human breast cance
N. tabacum CYCD3;1
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Result No.

Score

score greater t and is derived Pred. No.

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16 16 15 15 15 15 15 15

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Best Local S
Matches 16
                                                                                                                                                                                                                                                                                                   03-SEP-1997;
20-JUN-1997;
22-JUL-1997;
                  This sequence encodes a Borrelia burgdorferi (Bb) protein of the invention, which is suitable for use in a vaccine. The Bb polypeptides can be used in vaccines for eliciting protective antibodies to members the Borrelia genus, particularly for the use against Lyme disease in humans and animals. They can be used for preventing or attenuating an infection caused by a member of the Borrelia genus. The products can albe used for detection of members of the Borrelia genus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              products f caused by
                                                                                                                                                                                                                             Choi GH,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    B. burgdorfer1 antigenic protein coding sequence, f617.nt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAX61571;
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 Sequence
                                                                                                                       Claim 1;
                                                                                                                                         New isolated Borrelia burgdorferi nucleic acids - us products for the diagnosis, prevention and treatment caused by Borrelia, particularly Lyme disease
                                                                                                                                                                                                                                                                                                                                                   18-JUN-1998;
                                                                                                                                                                                                                                                                                                                                                                           30-DEC-1998
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                                                                                                                                                                                                                                                                                                                                                                                                                          Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                Antigenic protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAX61571 standard;
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                                                                                                                                                                                             P-PSDB;
                                                                                                                                                                                                                                                      (MEDI-)
                                                                                                                                                                                                                                                                                         22-JUL-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 humans and animals.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      invention, which
                                                                                                                                                                                                                                                                ( HUMA - )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   be used in vaccines for eliciting protective antibodies to members of Borrelia genus, particularly for the use against Lyme disease in lans and animals. They can be used for preventing or attenuating an ection caused by a member of the Borrelia genus. The products can also used for detection of members of the Borrelia genus.
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l Similarity 100.0%
l6; Conservative
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                                                                                                                                                                                                                                                      MEDIMMUNE INC
                                                                                                                                                                                                                                                                   HUMAN
 933
                                                                                                                                                                                                                                                                                                                                                                                                                         burgdorferi
                                                                                                                     Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                774 BP; 218 A; 74 C; 124 G; 358 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Page
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           for the diagnosis,
                                                                                                                                                                                                                             Erwin AL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Borrelia,
 ₿P;
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97US-0050359.
97US-0053344.
97US-0053377.
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 256
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                                                                                                                                                                                                                                                                                                                                                                                                                                              vaccine;
                                                                                                                    275pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     275pp;
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A; 90 C;
                                                                                                                                                                                                                             Hanson
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                                                                                                                    English.
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146 G;
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No.
441 T;
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0 other;
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diseases
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AAX20248
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Matches
                                                   Query Match
Best Local
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                                                                                             Sequence
                                                                                                                ∟уще
                                                                                                                         production of biosynthetic products, e.g. enzymes. Borrelia belongs to a family of motile, spiral-shaped bacteria called Spirochetes. Spirochetes are pathogenic in humans and Borrelia causes epidemic and endemic relapsing fever, and Lyme borreliosis, more commonly known as
                                                                                                                                                      AAX20248 to AAX20402 represent polynucleotide sequences isolated from Borrelia burgdorferi (Bb). Products derived from Bb can be used for the detection, diagnosis, characterisation, prevention and therapy of Bb infections, e.g. Lyme disease. They can also be used for the production of biosynthetic products, e.g. enzymes. Borrelia belongs
                                                                                                                                                                                                                      Claim 1;
                                                                                                                                                                                                                                                   New isolated Borrella burgdorferi nucleic acids - used to products for the detection, diagnosis, characterisation,
                                                                                                                                                                                                                                                                                  WPI; 1999-081217/07.
                                                                                                                                                                                                                                                                                                                  Clayton R,
                                                                                                                                                                                                                                                                                                                                                                                                                                             30-DEC-1998.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Borrelia burgdorferi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        epidemic relapsing fever; endemic relapsing fever; infection; diagnosis; characterisation; detection;
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20-JUN-1997;
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mes 16; Conserv
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                                         l Similarity
16; Conserv
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                                                                                             910715
                                                                                                                                                                                                                   Page 157-671; 1128pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              burgdorferi; spirochete;
                                         Conservative
                                                                                                                                                                                                                                                                                                                 Dougherty
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llarity 100.0%;
Conservative
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97US-0050359.
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Pred. No.
                                                                                             129646 C;
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No.
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tcagatttattttggg 587142

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RESULT
AAC50076
                                                                                          Query Match
Best Local Similarity 100.
                                                                                                                                                                                 The present sequence is the coding sequence for human thymic stromal lymphopoietin (TSLP). It was isolated by searching an EST library for sequences similar to the murine TSLP sequence. The protein is involved in the growth and differentiation of B and T cells. It can be used to study processes such as immune regulation, cell interaction and inflammatory responses. The nucleic acid can be used to identify human chromosome 5, to map genes along this chromosome, to identify genes on this chromosome which are associated with diseases, including Gardner syndrome and colorectal cancer, and to inhibit or induce B and T cell
                  AAC50076 standard; DNA; 1310
                                                                                                                                                                                                                                                                                                                           New human thymic stromal lymphopoietin (TSLP) polypeptide useful for stimulating lymphocyte development and proliferation
                                                                  4 gatttattttgggct 18
|||||||||||||||
721 GATTTATTTTGGGCT 707
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; thymic stromal lymphopoletin; TSLP; B cell maturation; immune regulation; cell proliferation; cell differentiation; cell d. cell migration; cell-to-cell interaction; inflammatory response; chromosome 5q21-22; Gardner syndrome; adenomatous polyposis coll; hereditary desmoid disease; Turcot syndrome; colorectal cancer; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human thymic stromal lymphopoietin (TSLP) coding sequence
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                                                                                                                   100.0%;
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                                                                                                                   Score 15;
Pred. No.
                  ВP
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                                                                                                        Mismatches
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     14 -MAY -1999

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19 -MAY 1999

20 -MAY 1999

21 -MAY -1999

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25 -MAY -1999

27 -MAY -1999

27 -MAY -1999

01 -JUN -1999

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09 -JUN -1999
 18-JUN-1999;
18-JUN-1999;
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06-MAY-1999;
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01-APR-1999;
06-APR-1999;
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05-MAY-1999;
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30-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-FEB-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana.
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990S-0139452

990S-0139453

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990S-0139460

990S-0139461
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990S-0132487.
990S-0132863.
990S-0134218.
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990S-0134219.
990S-013476.
990S-013476.
990S-013455.
990S-013553.
990S-0136529.
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990S-0136782.
990S-013722.
990S-013722.
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99US-0138847.
99US-0139119.
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990S-0130510.
990S-0130891.
990S-0131449.
990S-0132048.
990S-0132407.
990S-0132484.
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99US-0128714.
99US-0129845.
99US-0130077.
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18-JUN-1999; 18-JUN-1999; 18-JUN-1999;

99US-0139463. 99US-0139750. 99US-0139763.

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RESULT
AAC3778
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AC AA
AC AA
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AC AA
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DT 17
XX
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KW Hy
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                                                                                                                                                                                                  Query Match 62.5%; Strest Local Similarity 100.0%; Matches 15; Conservative 0;
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25-OCT-1999;
25-OCT-1999;
26-OCT-1999;
26-OCT-1999;
26-OCT-1999;
28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
Hybridisation assay; genetic mapping; gene expression control;
                    Arabidopsis thaliana DNA fragment SEQ ID NO: 18660
                                                                                                                         1290
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29-SEP-1
04-OCT-1
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27-AUG-1999;
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                                                          AAC37786;
                                                                          AAC37786 standard; DNA;
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13-OCT-1
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21-OCT-1999;
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21-OCT-1999;
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                                     (first entry)
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990S-0151233
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990S-0153758
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990S-0159631
990S-0160815
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990S-0161405
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99US-0151065.
99US-0151066.
                                                                           1313 BP
                                                                                                                                                          Score 15; DB 21; Length 1310; Pred. No. 15; 0; Mismatches 0; Indels
                                                                                                                                                         0;
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19-JUL-1999; 20-JUL-1999; 20-JUL-1999; 20-JUL-1999; 21-JUL-1999; 21-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999; 22-JUL-1999;

19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999; 19-JUL-1999;

990S-0139750 990S-0139891 990S-0140553 990S-0140553 990S-0140593 990S-0140823 990S-0142187 990S-0142187 990S-0142187 990S-014225 990S-014220 990S-014220 990S-014322 990S-014432 990S-014432 990S-014433 990S-014508 990S-014508

15-JUL-1999; 16-JUL-1999; 16-JUL-1999; 14-JUL-1999; 15-JUL-1999;

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9-JUL-1999; 2-JUL-1999; -JUL-1999

06-JUL-1999, 08-JUL-1999,

30-JUN-1 01-JUL-1

24-JUN-1999; 28-JUN-1999; 23-JUN-1999; 23-JUN-1999; 21-JUN-1999; 22-JUN-1999;

03-AUG-1999; 04-AUG-1999; 04-AUG-1999; 05-AUG-1999; 05-AUG-1999; 06-AUG-1999; 06-AUG-1999; 09-AUG-1999; 09-AUG-1999;

28-JUL-1999; 02-AUG-1999; 02-AUG-1999; 02-AUG-1999;

26-JUL-1999; 27-JUL-1999; 27-JUL-1999; 27-JUL-1999;

23-JUL-1999; 23-JUL-1999;

13-AUG-1 13-AUG-1 16-AUG-1 17-AUG-1 18-AUG-1 20-AUG-1 20-AUG-1 20-AUG-1 23-AUG-1 23-AUG-1 25-AUG-1

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990S-0147038
990S-0147204
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990S-0147303
990S-0147416
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Matches 15
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10-SEP-1999;
13-SEP-1999;
                            Porphorymonas gingivalis.
                                                             Porphorymonas gingivalis protein PG7 ORF encoding DNA.
                                                                                                        AAX91624 standard; DNA; 1392 BP
  17-JUN-1999
                W09929870-A1
                                           Porphorymonas gingivalis; PG; periodontal disease; gingivitis; vaccine; antigenic; ds.
                                                                              25-AUG-1999
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14-OCT-1999;
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15; Conserv
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99US-0161361.
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990S-0161404.
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99US-0159637
99US-0159638
99US-0159584
99US-0160741
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99US-0160770
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99US-0161993.
99US-0162142.
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99US-0159294.
99US-0159295.
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990S-0158029.
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990S-0153070.
990S-0153758.
990S-0154018.
990S-0154039.
990S-0154779.
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99US-0157753
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99US-0156596
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c; Pred. No. 15;
0; Mismatches
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110-DEC-1997;
31-DEC-1997;
30-JAN-1998;
10-MAR-1998;
09-APR-1998;
23-APR-1998;
23-APR-1998;
22-MAY-1998;
29-JUL-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAX91536 to AAX91801 encode two hundred and sixty six antigenic Porphorymonas gingivalis (PG) polypeptide sequences given in AAX34318 to AAX34583. AAX91802 to AAX91989 represent PCR primers used in the isolation of the PG polypeptides. The PG polypeptides have antibacterial activity with a vaccine mechanism of action. The PG polypeptides can be used as vaccines especially against Porphorymonas gingivalis. Probes can be used to detect Porphorymonas gingivalis in standard hybridisation assays. Porphorymonas gingivalis is involved in periodontal disease especially gingivitis.
mat_peptide
                           sig_peptide
                                                                    CDS
                                                                                                                                                    Human T1-receptor ligand III; T1-R ligand III; atherosclerosis; autoimmune disease; inflammation; metabolic dysfunction;
                                                                                                                                                                                      Human T1-receptor ligand III splice variant 1 encoding cDNA.
                                                                                                                                                                                                                                                                          AAV33461 standard; cDNA; 1836 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1392 BP; 361 A; 311 C;
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Ross BC,
                                                                                                            Homo sapiens.
                                                                                                                                                                                                                     10-DEC-1998
                                                                                                                                                                                                                                                AAV33461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; Page 156; 588pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Antigenic Porphorymonas gingivalis peptides for preventing gingivitis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1999-385613/32.
P-PSDB; AAY34406.
                                                                                                                                      immune-regulated disorder; ss.
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Rothel LJ,
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Conservative 0; Mix.
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97AU-000182
97AU-0001182
98AU-0001546
98AU-000264
98AU-0002911
98AU-0003128
98AU-0003538
98AU-0003538
98AU-0004917
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103..519
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31..102
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                                                                   Location/Qualifiers 31..522
                                                                                                                                                 inflammation; metabolic dysfunction;
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                                       "T1-R ligand III splice variant 1"
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                                                           08-JUL-1999;
11-JAN-2000;
02-MAY-2000;
                                                                                                                                                                                     Human; secretory protein; membrane protein; rheumatoid arthritis; diabetes; ss.
                    Ota T,
                                                                                                  07-JUL-2000; 2000EP-0114090
                                                                                                                                                                                                                                                                                  AAF93852 standard; cDNA; 2083 BP
WPI; 2001-093989/11
                                                                                                                         10-JAN-2001
                                                                                                                                              EP1067182-A2
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                      Human cDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1836 BP; 637 A; 306 C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 2; Fig 1; 115pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New human T1-receptor ligand III splice variant(s) - useful e.g. detecting and treating immune system related disorders cancer and inflammation
                                        (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           useful for screening agonists and antagonists. They are also claimed useful for treating disorders such as atherosclerosis, autoimmune disease, inflammation, metabolic dysfunction and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              variant
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DB; AAW70458.
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                   Isogai T,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ention provides novel human T1-receptor ligand III (T1-R III) splice variants and antibodies raised against these s. The present cDNA encodes the T1-R ligand III splice variants are claimed 1 protein. The T1-R ligand III splice variants are claimed
                                                                                                                                                                                                                 encoding a membrane or secretory protein clone PSEC0198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ni J,
                                                           99JP-0194179.
2000JP-0118775.
2000JP-0183766.
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                   Nishikawa
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Pred. No.
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                  Kawai Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                540 T; 0 other;
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15;
                 Sugiyama
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                                                                                                                                                                                             vaccine; gene therapy
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                Hayashi
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Matches
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                                                                                                              Sequence 2083 BP; 544 A; 467
                                                                                                                                                                                                                                                                                                                                                                                                                       protein/membrane protein expression. The nucleic acids and complementary sequences may also be used as DNA probes in diagnostic assays
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   can be used in gene therapy. The polynucleotide sequences and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate secretory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequences of the invention. The invention also includes methods for the production of antibodies directed against the proteins, and cDNA sequences, which can be used in vaccines. The polynucleotide sequences
                                                                                                                                                              arthritis
                                                                                                                                                                            be used as diagnostic agents for detecting the presence of the polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA). Examples of diseases which may be treated include rheumat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention relates to nucleic acid sequences AAF93744 - AAF93916 which encode human secretory or membrane proteins represented by AAB88317 - AAB88419. Included in the invention are primers AAF93917 - AAF94295 and AAF62232 - AAF62235 which are used to isolate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding secretory proteins/membrane proteins, useful in gene therapy or as candidate target molecules in drug development - \,
                                                                                                                                                                                                                                        activity. The antibodies and antagonists may also be used as therapeutic agents to down regulate expression and activity. The antibodies may also
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  l Similarity 100
15; Conservative
                       100.0%;
                                                62.5%;
    0;
                       Score 15;
Pred. No.
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                                                                                                              491 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                              581 T; 0 other;
                    DB
15;
                                                                                                                                                                            be treated include rheumatoid
                                           22;
  0;
                                           Length 2083;
  Indels
                                                                                                                                                                                                                                                                                                           assays to
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1309
AAA39981 standard; cDNA; 2385
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                                                    1 tcagatttattttgg 15
                                           tcagatttattttgg
                                            1323
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                                                                              CDS
                                                                                                                   TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; secreted protein; transmembrane protein; gene therapy; diagnosis; treatment; detection; ss.
                                                                                                                                                              Human TANGO 187 cDNA.
                                                                                                     Homo sapiens.
                                                                                                                                                                                               AAA39981;
                                               WO200018904-A2
                                                                                                                                                                              16-OCT-2000
                                                                                                                                                                             (first entry)
                                                                             Location/Qualifiers 386..1135
                                                              /*tag= a
/product= "TANGO 187
                                                                       /*tag=
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TANGO 185;
human; murine;
vaccine;

06-APR-2000

30-SEP-1998; 30-SEP-1999;

98US-0164220 99WO-US22817

02-OCT-1998;

98US-0164169

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                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes novel human and murine nucleic acids encoding CC TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. The polypeptides according to standard recombinant DNA methodologies. They CC may also be used to detect and quantify the presence of TANGO nucleic CC under also be used to detect and quantify the presence diseases associated with inappropriate TANGO expression (e.g. diseases related to over or CC under expression of the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides they encode may be used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a cc used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a CC may result in expression of an abnormally active notyperide That the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 may result in expression of an abnormally active polypeptide. The polypeptides may also be used to identify and produce agonists and antagonists of TANGO expression and activity which may be used to modulate TANGO related processes and diseases. The polypeptides are particularly useful for use as antigens for producing antibodies to TANGO proteins which may be used for inhibiting the activity of TANGO proteins. They may also be used to detect and quantify the presence of TANGO proteins in samples and therefore identify patients in whom the protein is over- or under-expressed. This sequence encodes the human TANGO 187 protein described in the method of the invention.
                                                                                                                                                                           TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 185; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; human; muj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1279 tcagatttattttgg 1293
                                                                                                                                            diagnosis; treatment;
                                                                                                                                                           secreted protein; transmembrane protein;
                                                                                                                                                                                                                                            Human TANGO 187-1/3 cDNA.
                                                                                                                                                                                                                                                                                                                                                               AAA39953 standard; cDNA; 2403 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 2385 BP; 623 A; 519 C;
                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                      16-OCT-2000
                                                                                                                                                                                                                                                                                                                              AAA39953;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inappropriate protein expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 tcagatttattttgg 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       62.5%; Score 15; 100.0%; Pred. No.
                                                                                                                                        detection; ss.
"TANGO 187-1/3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                588 G; 653 T; 2 other;
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15;
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                                                                                                                                                      numan; murine; vaccine;
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CC may also be used to detect and quantify the presence of TANGO nucleic CC acids in a sample and therefore identify or diagnose diseases associated CC with inappropriate TANGO expression (e.g. diseases related to over or CC under expression of the polypeptides or the expression of inactive CC polypeptides). The nucleic acids and the polypeptides they encode may be CC used according to standard gene therapy protocols, to treat diseases CC associated with inappropriate TANGO expression by supplementing a CC may result in expression of an abnormally active polypeptide. The CC may result in expression of an abnormally active polypeptide. The CC polypeptides may also be used to identify and produce agonists and CC antagonists of TANGO expression and activity which may be used to CC modulate TANGO related processes and diseases. The polypeptides are CC particularly useful for use as antigens for producing antibodies CC proteins. They may also be used for inhibiting the activity of TANGO proteins in samples and therefore identify patients in whom the CC TANGO proteins in samples and therefore identify patients in whom the CC protein is over- or under-expressed. This sequence encodes the human CC TANGO 187-1/3 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucle acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 polypeptides according to standard recombinant DNA methodologies. They
Sequence 2403 BP; 660 A; 504 C; 566 G; 673 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 1c; Fig 20; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein expression -
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02-OCT-1998;
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98US-0164169
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Best Local Similarity
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TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; secreted protein; transmembrane protein; gene therapy;
                                                                                                                                                               1285
                                             Human TANGO 187-2 cDNA
                                                                  16-OCT-2000
                                                                                        AAA39979;
                                                                                                         AAA39979 standard; cDNA; 2418
                                                                                                                                                                                 1 tcagatttattttgg 15
                                                                                                                                                             tcagatttattttgg 1299
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                                                               (first entry)
                                                                                                                                                                                                                 62.5%;
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Pred. No.
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                       TANGO 185;
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0;

vaccine;

human; murine;

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                    AAA39975
                                     RESULT
                                                                                                                                                                                                                                                        cc polypeptides according to standard recombinant DNA methodologies. They
CC may also be used to detect and quantify the presence of TANGO nucleic
CC acids in a sample and therefore identify or diagnose diseases associated
CC with inappropriate TANGO expression (e.g. diseases related to over or
CC under expression of the polypeptides or the expression of inactive
CC polypeptides). The nucleic acids and the polypeptides they encode may be
CC used according to standard gene therapy protocols, to treat diseases
CC associated with inappropriate TANGO expression by supplementing a
CC patients own production of the polypeptide of to rectify mutations that
CC may result in expression of an abnormally active polypeptide. The
CC polypeptides may also be used to identify and produce agonists and
CC antagonists of TANGO expression and activity which may be used to
CC modulate TANGO related processes and diseases. The polypeptides are
CC particularly useful for use as antigens for producing antibodies
CC to TANGO proteins which may be used for inhibiting the activity of TANGO
CC TANGO proteins which may be used for inhibiting the activity of TANGO
CC TANGO proteins in samples and therefore identify patients in whom the
CC TANGO 187-2 protein described in the method of the invention.
                                                                                                                                                     Matches
                                                                                                                                                                       Query Match
Best Local
                                                                                      . 1312
AAA39975 standard; cDNA; 2490 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215
                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein expression -
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02-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           diagnosis; treatment;
                                    13
                                                                                                                                                                   Local
                                                                                                                 1 tcagatttattttgg 15
                                                                                                                                                    Similarity
15; Conserv
                                                                                                                                                                                                                               2418 BP; 631 A; 528 C; 594 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fig 50;
                                                                                                                                                    Conservative
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98US-0164169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag=
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                                                                                                                                                                 62.5%;
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Matches Query Match Best Local :

15;

Conservative

0;

Similarity

62.5%; Score 15; 100.0%; Pred. No.

ore 15; DB; red. No. 15; Mismatches

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Indels

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Gaps

0

21;

Length 2490;

Sequence

2490

BP;

642 A;

548 C;

626 G;

669

T; 5

other,

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peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 polypeptides according to standard recombinant DNA methodologies. They may also be used to detect and quantify the presence of TANGO nucleic acids in a sample and therefore identify or diagnose diseases associated with inappropriate TANGO expression (e.g. diseases related to over or under expression of the polypeptides or the expression of inactive polypeptides). The nucleic acids and the polypeptides they encode may be used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a pattents own production of the polypeptide of to rectify mutations that may result in expression of an abnormally active polypeptide. The polypeptides may also be used to identify and produce agonists and antagonists of TANGO expression and activity which may be used to modulate TANGO related processes and diseases the polypeptide.
                                  modulate TANGO related processes and diseases. The polypeptides are particularly useful for use as antigens for producing antibodies to TANGO proteins which may be used for inhibiting the activity of TANGO proteins. They may also be used to detect and quantify the presence of TANGO proteins in samples and therefore identify patients in whom the protein is over- or under-expressed. This sequence encodes the human TANGO 187-1 protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        This invention describes novel human and murine nucleic acids encoding TANGO polypeptides (which are either wholly secreted or transmembrane proteins) which can be used for gene therapy and/or vaccination. The peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TANGO 180; TANGO 181; TANGO 182; TANGO 183; TANGO 184; TANGO 186; TANGO 188; TANGO 189; TANGO 215; TANGO 187; secreted protein; transmembrane protein; gene therapy; diagnosis; treatment; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 46; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-293144/25.
P-PSDB; AAY88295.
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02-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inappropriate protein expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MILL-) MILLENNIUM BIOTHERAPEUTICS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     30-SEP-1999;
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98US-0164169
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386..1240
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This invention describes novel human and murine nucleic acids encoding CC TANGO polypeptides (which are either wholly secreted or transmembrane CC proteins) which can be used for gene therapy and/or vaccination. The CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic CC acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215. They CC may also be used to detect and quantify the presence of TANGO nucleic CC with inappropriate TANGO expression (e.g. diseases related to over or CC under expression of the polypeptides or the expression of inactive CC used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a cC used according to standard gene therapy protocols, to treat diseases associated with inappropriate TANGO expression by supplementing a cC may result in expression of an abhormally active polypeptide. The CC particularly useful for use sed to identify and produce agonists and cc modulate TANGO expression and activity which may be used to condulate TANGO proteins which may be used for inhibiting the activity of TANGO CC TANGO proteins which may be used for inhibiting the activity of TANGO CC TANGO proteins in samples and therefore identify the presence of TANGO protein is over- or under-expressed. This sequence encodes the human cc TANGO 187-1/2 protein described in the method of the invention.
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TANGO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 49; 249pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with inappropriate protein expression -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAY88298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2000-293144/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Barnes TM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; transmembrane protein; gene therapy; vaccine,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-OCT-2000
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98US-0164169
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BP; 650 A; 557 C; 632 G; 679 T; 5 other;

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AAA39980
ID AAA3
This invention describes novel human and murine nucleic acids encoding CC TANGO polypeptides (which are either wholly secreted or transmembrane CC proteins) which can be used for gene therapy and/or vaccination. The CC peptides are designated TANGO 180 to TANGO 189 and TANGO 215. The nucleic CC acids may be used to produce TANGO 180 to TANGO 189 and TANGO 215 CC polypeptides according to standard recombinant DNA methodologies. They CC may also be used to detect and quantify the presence of TANGO nucleic CC with inappropriate TANGO expression of the polypeptides or the expression of inactive CC under expression of the polypeptides or the expression of inactive CC used according to standard gene therapy protocols, to treat diseases CC associated with inappropriate TANGO expression by supplementing a CC patients own production of the polypeptide of to rectify mutations that CC may result in expression of an abnormally active polypeptide. The CC modulate TANGO expression and activity which may be used to condulate TANGO related processes and diseases. The polypeptides are
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1417 tcagatttattttgg 1431
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isolated nucleic acids encoding TANGO polypeptides useful for preventing, diagnosing and treating diseases associated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAY88300
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02-OCT-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human TANGO 187-3 cDNA.
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Result
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Perfect score:
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2000 Compugen Ltd
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
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US-08-851-968-5
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US-08-9315-793-51
US-09-315-793-51
US-07-638-431-1
PCT-US92-00018-1
US-08-431-33
US-08-431-33
US-08-6431-319A-3
US-08-631-319A-3
US-08-631-319A-3
US-08-631-319A-3
US-08-631-319A-3
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US-08-631-319A-3
US-08-838-973B-15
US-08-980-329C-1
US-09-100-664A-1
US-09-040-485-1
US-08-551-723B-4
US-08-551-723B-4
US-08-714-918-8
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US-09-085-273-40	US-08-796-101-4	US-08-658-665-40	US-09-079-587-5	US-08-816-155B-5	US-08-815-809-3	US-08-971-988-1	US-08-588-985-1	US-08-611-729A-1	US-08-400-159-1	US-08-566-398-16	US-08-417-210A-80	US-09-123-465-3	US-08-555-723B-3	US-08-391-743A-1	US-09-356-952-13	US-07-842-165-5	US-08-475-427-5
40,	Sequence 4, Appli	Sequence 40, Appl	Sequence 5, Appli	5	ω.	_	-	1,	Sequence 1, Appli	16,	Sequence 80, Appl	Sequence 3, Appli	ω	1,	Sequence 13, Appl	Sequence 5, Appli	Sequence 5, Appli

US-08-793-410-11

ALIGNMENTS

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Sequence 1 Patent No.
                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/793,410
FILING DATE:
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/10627
FILING DATE: AUGUST 25, 1995
ATTORNEY/AGENT INFORMATION:
NAME: CHRISTENBURY, LYNNE M.
REGISTRATION NUMBER: 30,971
REFERENCE/DOCKET NUMBER: CR-9567-A
                                                                                                                                                 TELEFAX: 302-773-0164
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
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TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.50 INCH
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MICROSOFT WINDOWS 95
SOFTWARE: MICROSOFT WORD VERSION 7.0A
CURRENT APPLICATION DATA:
                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 302-992-5481
TELEFAX: 302-773-0164
             MOLECULE TYPE: D
HYPOTHETICAL: NO
                                                                                                                               SEQUENCE CHARACTERISTICS:
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ADDRESSEE: E. I. DU
ANTI-SENSE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                     LENGTH: 1303 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: WILMINGTON
STATE: DELAWARE
COUNTRY: USA
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5. 5955650
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1007 MARKET STREET
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                                 DNA (genomic)
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US-08-506-864A-5/c
                                                                    Query Match
Best Local Similarity
                                                        Matches
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NFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches,
                                                                                                                                                                                                                                      ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA
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                                                                                                                                                                                     FEATURE:
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APPLICANT: : FUJIWARA, YOSI
164 ATTTTGGGCTTCAC 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                              ELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: MS-DOS 5
SOFTWARE: WORDPERFECT 5.0
                                                                                                                                   IDENTIFICATION METHOD: experimental examination
                                                                                                                                                       LOCATION:
                                                                                                                                                                                               LIBRARY:
                                                                                                                                                                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                              STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                 TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: JP6-1 FILING DATE: 29-JULY-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                9 attttgggcttcac 22
                                                                                                                                                                   NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/506,864A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 tttättttgggcttc
                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                          ENGTH:
                                                        14;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         49008-1699
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kalamazoo
                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                       Terryence F. Chapman RATION NUMBER: 32549
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Michigan
                                                                                                                                                                                            human DNA cosmid library
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2026 Rambling Road
                                                                                                                                                                   exon
                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                         Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IBM PC/XT/AT Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FLYNN, THIEL, BOUTELL & TANIS, P.C.
                                                                                                                                                                                                                                                                                                                                                                  (616)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUJIWARA, YOSHIYUKI
WIION: PRLTS PROTEINS AND DNA'S
WIION: ENCODING THE SAME
                                                                                                                                                                                                                                                   genomic DNA
                                                                                                                                                                                                                                                                               double
                                                                                                                                                                                                                                                                                                                                                                 381-1156
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100.0%;
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                                                                                 58.3%;
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                                                                 Score 14;
Pred. No.
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Pred. No.
                                                      Mismatches
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                                                                              DB 2; Length 486;
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3.5;
                                                   0; Indels
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RESULT 4 US-09-484-345-10 ; Sequence 10, Ap

Patent No.

INFORMATION:

Application US/09484345

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APPLICANT: Robert McKay APPLICANT: Alexander H. Bo: APPLICANT: Brenda F. Baker

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                                                                                                                                           US-08-851-968-5
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US-08-851-968-5/c
                                                            Query Match 58.3%;
Best Local Similarity 100.0%;
Matches 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (616) 381-5465
INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 49008-1002
ZIP: 49008-1002
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches,
MEDIUM TYPE: DISKette, 3.5 inches,
COMPUTER: IBM PC/XT/AT Compatible
COMPUTER: SYSTEM: MS-DOS 5.0
                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE: (616) 381-1156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER:.. JP6-178131
FILING DATE: 29-JULY-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
164 ATTTTGGGCTTCAC 151
                                                                                                                                                                                                                                    MMEDIATE SOURCE:
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APPLICANT: : FUJIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                       LOCATION: 74..371
IDENTIFICATION METHOD:
                                                                                                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME: Terryence F. Chapman REGISTRATION NUMBER: 32549
                                                                                                                                                                                      NAME/KEY: exon 3
                                                                                                                                                                                                                     LIBRARY:
                                                                                                                                                                                                                                                                                                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Kalamazoo
                           9 attttgggcttcac 22
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                                                                                                                                                                                                                                                                                                                                                  ENGTH: 486
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                                                                                                                                                                                                                                                                                                                                nucleic acid
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                                                                                                                                                                                                                                                                                  genomic DNA
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                                                                                                                                                       experimental examination
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                                                                           Score 14; DB; Pred. No. 13;
                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                         Furuya Case 1334
                                                           Mismatches
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                                                                                       Length 486;
                                                           Indels
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US-08-506-864A-2/c
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; NAME/KEY: CDS
; LOCATION: (859)...(940)
US-09-484-345-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08506864A Patent No. 5834245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQ ID NO 10
                                                                                                                                                             TELEFAX: (616) 381-546 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/484,345
CURRENT FILING DATE: 2000-01-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: ANTISENSE MODULATION OF PEROXISOME PROLIFERATOR-ACTIVATED RECEPTOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE: RTS-0104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQ ID NOS: 90
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Homo sapiens
                                                                                                                                                                                                    REFERENCE/DOCKET NUMBER: Furuya Case 1334
TELECOMMUNICATION INFORMATION:
TELEPHONE: (616) 381-1156
                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 49008-1699

ZIP: 49008-1699

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches,
COMPUTER: IBM PC/XT/AT Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                 MOLECULE TYPE: (
                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                 ORGANISM:
                                                                                                                                     TYPE: nucleic acid
                                                                                                                                                                                                                                                   REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: JP6-1 FILING DATE: 29-JULY-1994
                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
               NAME/KEY:
                                         LIBRARY:
                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER:
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                                      human fetal lung cDNA library
               CDS
                                                                   Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLYNN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FUJIWARA,
                                                                                           cDNA to mRNA
                                                                                                                                                                          6) 301
381-5465
NO: 2:
                                                                                                                         double
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100.0%;
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
  Query Match 58.3
Best Local Similarity 100.
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. 5935786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best
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                                                                                                                                                                                                                                                                                  TELEFAX: (616) 381-54
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                FEATURE
                                                                                                                                                                                  ORIGINAL SOURCE:
                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 29-JULY-199 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: WordPerfect 5.0 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
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                                                                                                  NAME/KEY:
LOCATION:
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                                                                                                                                                                                                              STRANDEDNESS:
TOPOLOGY: 11
                                                                                                                                          LIBRARY:
                                                                                                                                                                      ORGANISM:
                                                                                                                                                                                                                                                                                                           TELEPHONE:
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                                                                                     IDENTIFICATION METHOD:
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62..1189
                                                                                                                                            human
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                                                                                                                                                                                                                                                                                                            (616) 381-1156
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30: 2:
58.3%; 5cc
100.0%; Pr
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100.0%;
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                 Score 14;
Pred. No
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218

Matches

Sequence

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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inches.
COMPUTER: IBM PC/XY/AT Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/08851968
                                                   fetal lung cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRLTS PROTEINS AND DNA'S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ENCODING THE SAME
                                                                                                                                                                                                                                                                                                                              JP6-178131
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experimental examination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3.5 inches,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              experimental examination
                                                                                                                                                                                                                                                        Furuya Case 1334
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BOUTELL & TANIS, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 14;
Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.44 Mb storage
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Mismatches

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Length 1502;

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                                                                                                                            RESULT
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           GENERAL INFORMATION:
APPLICANT: Roberts, C
TITLE OF INVENTION: E
TITLE OF INVENTION: E
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                                                                           Sequence 51, Application US/09315793 Patent No. 6221597
                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: (303) 499-80: INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                     HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISH: Caenorhabditis elegans
IMMEDIATE SOURCE:
CLONE: SPE-4
                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION: NAME: Ferber, Donna M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Soulder
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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| 207 ATTTTGGGCTTCAC 194
                                                                                                                                                                                                                                     Local Similarity 100 es 14; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
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REFERENCE/DOCKET NUMBER: 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 24-JAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                     not relevant
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (303) 499-8080
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Christopher J.

ESSENTIAL GENES OF YEAST AS TARGETS FOR ANTIFUNGAL
AGENTS, HERBICIDES, INSECTICIDES AND ANTI-PROLIFERATION
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                                                                                                                                                                                                                                                    58.3%; Score 14; 100.0%; Pred. No
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Best Local S
Matches 14
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CURRENT FILING DATE: 1999-05-21
NUMBER OF SEQ ID NOS: 62
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 51
LENGTH: 3282
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILE REFERENCE:
                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                             NAME: Spevack, Avrom D. TELECOMMUNICATION INFORMATION: TELEPHONE: (301) 295-6759
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: PatentIn Release #1.24
CURRENT APPLICATION DATA:
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                                                                                    ORIGINAL SOURCE:
                                                                                                  HYPOTHETICAL:
ANTI-SENSE: N
                                                                                                                            MOLECULE TYPE:
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MMEDIATE SOURCE
                                            AIGINAL PIUL
ORGANISM: PIUL
17X(NL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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                        TISSUE TYPE:
                          DEVELOPMENTAL STAGE: TISSUE TYPE: Blood
                                                                                                                                              TOPOLOGY:
                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                       TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CITY: Bethesda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET:
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                                                                                                                                                                                      LENGTH:
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NMRDC Building 1 T-12 National Naval
Medical Center
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                                                                    Plasmodium yoelii
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Khusmith, Srisin
                                                                                                                                             linear
            erythrocytic stage
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                                                                                                                            DNA (genomic)
                                                                                                                                                            double
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                                      erythrocytic stage
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; LOCATION: 718..31
; OTHER INFORMATION:
US-07-638-431-1
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Best Local Similarity
                                                                                                                                                                                                                                                             TELEFAX: (301) 295-4033
NFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 4673 base pairs
                                                                                                                                                           HYPOTHETICAL: N
ANTI-SENSE: N
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Spewack, Avram D.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 295-6759
                                                                                                                                                                                         TOPOLANDI TYPE: DI
                              FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION DATA:
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                                                                                                                        ORGANISM: Plasmorrow 17X(NL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                      MMEDIATE SOURCE:
                                                                   TISSUE TYPE: Blood
TOTAL TYPE: erythrocytic stage
                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC CC
OPERATING SYSTEM: F
SOFTWARE: Patentin
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US92/00018
FILING DATE: 19920103
CLASSIFICATION: 424
                                                                                                    DEVELOPMENTAL STAGE:
TISSUE TYPE: Blood
                                                         LIBRARY:
                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                     TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 20814-5044
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FOCATION: 718..3195
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                                        : Py-lambdagt11-2-7 kb genomic expression Py10.1111
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Py10.1111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Medical Center
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NMRDC Building 1 T-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
                                                                                                                                             Plasmodium yoelii
                                                                                                                                                                                                  linear.
E: DNA (genomic)
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Khusmith, Srisin
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                                                                                                                                                                                                                                       double
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 Release #1.24
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                                                                                                                erythrocytic stage
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Pred. No.
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13;
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                                 US-08-488-271B-33/c
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   Sequence 33, Application US/08488271B Patent No. 5892013
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US-08-479-275D-33
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                                                             Matches
                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 58.3%; Score 14;
Best Local Similarity 100.0%; Pred. No.
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1375 TATTTTGGGCTTCA 1362
                                                                                                                                             TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 23 base pairs
                                                                                                                                                                                                                                                               TELEPHONE: 212-867-0123
                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 510
ATTORNEY/AGENT INFORMATION:
NAME: Lambiris, Elias J.
                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: LIPASE VARIANTS
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11 tttgggcttcact 23
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|14 TTTGGGCTTCACT 2
                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: FILING DATE: 07-JU
                                                                                                                                                                                         TYPE: nucleic acid
                                                                                                                                                                                                                                                             TELEPHONE:
                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     405 Lexington Avenue, Suite 6400
                                                                                                                                                                                                   23 base pairs
                                                                                                                                                                                                                                                 212-878-9655
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Thellersen, Marianne
                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gormsen,
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                                                                      54.2%; Score 13; 100.0%; Pred. No.
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                                                          Mismatches
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13;
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US-08-631-319A-3
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                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/08631319A Patent No. 6117641
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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                                                                                                                                                                                                                                          APPLICANT:
APPLICANT:
APPLICANT:
           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS
                                                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                      TITLE OF INVENTION: Assay and Reagents for Identifying Anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                           UMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
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                                                                               COUNTRY: USA
ZIP: 02109
                                                                                                                                             STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
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REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08 FILING DATE: 07-JUNE-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  23 base pairs
                                                                                                                                           ONE POST OFFICE SQUARE

    No. 5892013o No. 5892013disk of No. 5892013th America,
    Lexington Avenue, Suite 6400

                                                                                                                                                                                                                                        Levin, David
Ohya, Yoshikazu
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ASCII (text)
                                                                                                                                                            FOLEY,
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Best Local :
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TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 3:
INFORMATION FOR SEQ ID NO: 17
SEQUENCE CHARACTERISTICS
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NAME: Pham, Chinh H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                         CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,306B
FILING DATE: 23-Apr-1997
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                 ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 617-832-1000
                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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ADDRESSEE: FOLEY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 48
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nucleic acid
                                                                                                                                                               APPLICATION NUMBER: US 08/771,212
FILING DATE: 20-DEC-1996
APPLICATION NUMBER: US 08/631,319
FILING DATE: 11-APR-1996
                                                                                     NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-074.04
                                                                                                                                                                                                                                                                                                                   SOFTWARE: WordPad
                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Boston
                                    TELEFAX: 617-832-7000
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: One Post Office Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING
ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
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Ohya, Yoshikazu
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Gaps

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Query Match
Best Local Similarity 100.0
Watches 13; Conservative
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US-08-838-973B-15
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STRANDEDNESS: single

TOPOLOGY: linear.

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 17:

US-08-842-306B-17
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GENERAL INFORMATION:
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Best Local Similarity 100
Matches 13; Conservative
                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-832-1000
TELEPAX: 617-832-7000
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC COMPACTIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PALENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/838,973B
FILING DATE: 23-Apr-1997
PRIOR APPLICATION UNDBER: US 08/631,319
APPLICATION NUMBER: US 08/631,319
FILING DATE: 10-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-074.05
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ZIP: 02109-2170
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY, HOAG & ELIOT LLP
STREET: One Post Office Square
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Berlin, Vivian
Damagnez, Veronique
Smith, Susan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS, AND USES RELATED THERETO
                                                                                                                                                                                                                                           LENGTH: 42 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
                                                   54.2%; Score 13; DB 4; Length 42; 100.0%; Pred. No. 43; ative 0; Mismatches 0; Indels
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100.0%; Pred. No.
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Search completed: November 15, 2001, 05:55:52 Job time: 6743 sec

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gb_est90:

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em_gss_other:*
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gb_est106:*

gb_est103:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

em_gss_rod8:* gb_gss35:* gb_gss36:* gb_gss37:*

em_gss_inv4:*
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                                                                AUTHORS
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                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; 1 (bases 1 to 426)
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                  1 (bases 1 to 406)
Bonaldo, M.F., Lenno
                                                                       Norway rat.
Rattus norvegicus
Eukaryota; Metazoa;
Normalization and subtraction: two approaches
                                                   Rattus
                                                                                                                                    EST
                                                                  Mammalia; Eutheria;
                                                                                                                                                 AW528260.1
                                                                                                                                                                  AW528260
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Tel: 801 585 5606
Fax: 801 585 7177
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University of Utah
University of Utah
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="Male"
                                                                                                                                                GI:7170674
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100.0%; Pr
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                  Lennon, G. and Soares, M.B.
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TITLE
                                                                                                                                                                                  AW528260 406 bp mRNA EST 06-MAR-2000 UI-R-BT1-ajw-e-04-0-UI.S1 UI-R-BT1 Rattus norvegicus cDNA clone UI-R-BT1-ajw-e-04-0-UI 3', mRNA sequence.
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Class: plasmid ends
High quality sequence stop: 426.
Location/Qualifiers
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Seq primer: CACACAGGAAACAGCTATGACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: ddunn@genetics.utah.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with 74 DNA polymerase and 74 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptored DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gil4732114|gb\AF129072.1), a copy-number inducible derivative of plasmid R1. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /Note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (http://www.jax.org/resources/documents/dnares/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Mouse 10kb plasmid UUGC1M library"
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/clone="UUGC1M0201G13"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Mus musculus
/strain="C57BL/6J"
Chordata; Craniata; Vertebrata; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae;
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Pred. No.
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REFERENCE
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Best Local :
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1 (bases 1 to 591)

Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. a
                                                                                                                                                                                                                           AQ705173 591 bp DNA
HS_5520_B1_E02_T7A RPCI-11 Huma
genomic clone Plate=1096 Col=3
                                                                                                                                                                       SSD
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Hood, L.
                                                                                                                                                                                         AQ705173.1
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                                                                                                                        Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: msoares@blue.weeg.uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tel: 319 335 8250 Fax: 319 335 9565
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University of Iowa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Vector: pT/T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The library UI-R-BT1 is a subtracted library derived from a mixture of the following tissues: hippocampus, thalamus, mid-brain, medulla, corpus striatum, cerebral cortex and testis. For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TAG_TISSUE=corpus-striatum
TAG_SEQ=CTAGG"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     medulla, corpus striatum, cerebral cortex and testis. For a detailed description of the library from which this clone was derived, please visit our web site at ratest.eng.uiowa.edu. The subtraction has been previously
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/clone_lib="UI-R-BT1"
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/db_xref="taxon:10116"
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TITLE
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                                                                                                                                                                                                                     Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                            Contact: Robert Strausberg, Ph.D. Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 159)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering.bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
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(206) 616-3887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ECORI Methylase. Size SEASULES PARCES.6 vector at ECORI sites PARCES.6 vector at ECORI sites 137 c 103 g 216 t
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/sex="male"
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                                                                                                                                                                                                                                                                      Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
Clones are derived from the human BAC library RPCI-11. For BAC
Library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (intp://bacpac.com). BAC end search page:
                                                                                                                                                                                                                                                           http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
                                                                                                                                                                                                                                                                                                                                                                                                                               9712 Medical Center Dr., Rockville,
                                                                                                                                                                                                                                                                                                                                                                                                                                                Department of Eukaryotic Genomics
The Institute for Genomic Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Mark Adams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Other_GSSs: RPCI11-68J13.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Adams, M.D., Rounsley, S.D., Zhao, S., Bass, S., Linher, K., Golden, K., Berry, K., Granger, D., Suh, E., Wible, C., de Jong, P. and Venter, J.C. Use of human BAC End Sequences for Sequence-Ready Map Building
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ237895 210 bp DNA 655 21 at a fr 277 RPCI11-68J13.TK RPCI-11 Homo sapiens genomic clone RPCI-11-68J13,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (1998)
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/Cell_type="Lymphocytes"
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2:
RPCI11 Human Male BAC Library"
20 c .32 g 71 t 2 others
                                                                                                                  /organism-"Homo sapiens"
/db_xref="GDB:7525956"
/db_xref="taxon:9606"
/clone="RPCI-11-68J13"
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27 c 23 g 56 t
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/clone="IMAGE:912592"
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/lab_host="DH10B"
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BB528140
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16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (infoeimage.linl.gov) for further information.
Insert Length: 421 Std Error: 0.00
Seq primer: -400P from Gibco.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A1914472 266 bp mrNA EST 17-DEC-1 wdd49e06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2331490 3' similar to 9b:X63547_cds2 UBIQUITIN CARBOXYL-TERMINAL HYDROLASE TRE-2 (HUMAN);, mRNA sequence. A1914472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tumor Gene Index 
Unpublished (1997)
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1 (bases 1 to 266)
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AI914472.1 GI:5634327
                                                                                                                                                                                                                                                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                      /note-*Organ: pooled; Vector: pT773D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NbHL19W, testis NHT, and B-cell NCI_CGAP_GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 682632-687339, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo. **
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268 bp mRNA EST 28-JUL-2000 RIKEN full-length enriched, 15 days embryo head Mus cDNA clone D930045A20 3', mRNA sequence.
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/db_xref="taxon:9606"
/clone="IMAGE:2331490"
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/lab_host="DH10B"
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                                                                                                                                                                                                                                                                                                 66.7%; Score 16; DB 103; 100.0%; Pred. No. 1.1e+02;
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                                                                                                                                                                                                                                                                             Mismatches
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1.1e+02;
thes 0;
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Thermostabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y., and Hayashizaki,Y.
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URL:http://genome.rtc.riken.go.jp/
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3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel: +81-298-36-9013
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
                                                                   prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'
                                                                                                                                                                                                                                                                   /note="Site_1: Sal1; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was
                            primed with a primer [5' GAGAGAGAGAGAGACCCATTTTTTTTTTTTTTTTTTYN 3'], cDNA was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /tissue_type="head"
/dev_stage="15 days embryo"
/lab_host="DH10B"
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/clone="p930045A20"
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/strain="C57BL/6J"
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the XhoI and BamHI sites. Vector: a
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URL.http://genome.rtc.riken.go.jp/
Carninci.P., Nishiyama,Y., Westover,A.,
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Tel: +81-298-36-9013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Genome Exploration Research Group, Life Science Tsukuba Center, Genome Science Laboratory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BB473121 289 bp mRNA EST 22-JUL-2000 BB473121 RIKEN full-length enriched, 12 days embryo eyeball Mus musculus cDNA clone D230049L08 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: +81-298-36-9098
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sciences Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Yoshihide Hayashizaki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RIKEN Mouse ESTs (Konno, H., et al.)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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                                                                                                                                                                                                                                                                details
                                                                                                                                                                                                                                                                                 visit our web site (http://genome.rtc.riken.go.jp) for
                                                                                     /organism="Mus musculus"
/db_xref="taxon:10090"
                                              /clone="D230049L08"
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    /clone_lib="RIKEN full-length enriched,
                                                                                                                                                                                                                 Cocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 16; DB 160; Pred. No. 1.1e+02;
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12 days embryo
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                                                                                                                                                                              Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                      White,Y., Wylie,T., Waterst
                                                                                                                                                                                                                                                                                                                                                                Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin, J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Materston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                Hillier, L., Allen, M., Bowles, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 294)
                                                                                                                                                                                                                                                                                           Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                             Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                          Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   zp01g06.r1 Stratagene ovarian cancer (#937219) Homo sapiens cDNA
clone IMAGE:595162 5', mRNA sequence.
                                                                                                                                                                         High quality sequence stop: 260.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
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/dev_stage="adult, 64 years"
/lab_host="SOLR (kanamycin resistant)"
/note="Vector: Bluescript SK-; Site_1: EcoRI; Site_2: XhoI
/note="Vector: Bluescript SK-; Primer: Oligo dT. Papillary
                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:595162"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone_lib="Stratagene ovarian
                                                                    /sex="female"
                                                                                                                                                           location/Qualifiers
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/lab_host="DH10B"
/note="Site_1: Sal1; Site_2: BamH1; cDNA library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="eyeball"
/dev_stage="12 days em]
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                                                                               cancer (#937219)"
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Query Match Best Local S Matches 16

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                                                                                                                                                                                                                                                                                                                                     Email: egreen@nhgri.nih.gov
Plate: 11 row: G column: 05
Seq primer: -21M13 (ABI).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                            Genome Technology Branch
National Human Genome Research Institute/NIH
49 Convent Dr., MSC4431, Building 49, Room 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2006 expressed-sequence tags derived from human chromosome 7-enriched cDNA libraries Genome Res. 7 (3), 281-292 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16;
                                                                                                                                                                                                                                                                                                                                                                                                                  Fax: 3014024735
                                                                                                                                                                                                                                                                                                                                                                                                                                    Tel: 3014020201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Eric D. Green
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Touchman, J.W., Bouffard, G.G., Weintraub, L.A., Idol, J.R., Wang, L., Robbins, C.M., Nussbaum, J.C., Lovett, M. and Green, E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 295)
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7B11G05 Chromosome
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                63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107
           /sex="female and male mixture"
/tissue_type="brain"
/tissue_type="brain"
/dev_stage="pool of 9 week and 12 week"
/lab_host="E. coli strain DH5 alpha"
/note="Organ: brain; Vector: pampl0; cDNA was generated from cytoplasmic RNA using a mixture of random DNA hexamers and oligo(dT). From this pool of cDNA, human chromosome 7-enriched cDNA was isolated by direct cDNA selection using chromosome 7 genomic DNA (cosmids). The resulting direct-selected cDNA was cloned into a plasmid vector using a non-directional uracil DNA glycosylase (UDG)-mediated cloning strategy."

63 a 56 c 76 g 93 t 7 others
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                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="7B11G05"
                                                                                                                                                                                                                                                                                                                          1. .295
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DSOMe 7 Fetal Brain cDNA Library Homo sapiens cDNA
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hes 0;
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         7 others
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GATTTATTTTGGGCTT 181

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SOURCE
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AUTHORS
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Best Local
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                                          Mus musculus
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                  AU040896
AU040896
                        õ
                                                                                                          EST
                                                                                                                         AU040896.1
                                                                                                                                                AU040896 427 bp mRNA
AU040896 Mouse four-cell-embryo
J0820C10 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                             . Similarity
16; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A1079841 337 bp mRNA EST 28-AUG-1998 ox50d02.x1 Soares_total_fetus_Nb2HF8_9w Homo sapiens cDNA clone IMAGE:1659747 3', mRNA sequence.
                                                                                             house mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST.
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1 (bases 1 to 337)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  human.
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(bases 1 to 427)

,M.S.H., Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., D
Liang,Y., Kargul,G.J., Sharara,R., Lim,M.K. and Doi,H.
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                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                        Double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pTT3 vector. Library went through one round of normalization, and was constructed by Bento Soares and M. Fatima Bonaldo. " 63 c 51 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab_host="DH10B"
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/dev_stage="8-9 weeks"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /clone="IMAGE:1659747"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                        GI:3954720
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                                                                                                                                                                                                                                                                                                                        Score 16;
Pred. No.
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                                           Craniata; Vert
Sciurognathi;
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hes 0;
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                                                             Vertebrata; Euteleostomi;
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                                                                                                                                                               musculus
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                                              Muridae;
                  Sun, T., DePalma, G.E
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                                             Murinae;
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AU017418/c
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Local
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                                                                                                             16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (1998)
Contact: Hirofumi Doi
Doi Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Ch
Email: hd@bioa.jst.go.jp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        KO,M.S.H. Kitchen,J.R., Wang,X., Threat,T.A., Sun,T., DePalma,G.E., Liang,Y., Kargul,G.J., Sharara,R. and Doi,H.
Systematic analyses of genes expressed in 2-cell stage mouse embryos (The ERATO/Doi Project at Wayne State University) (Ko,M.S.H. et al.)
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AU017418
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AU017418
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus
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Dol Bioasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba
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ERATO/Doi Project at Wayne
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                                                                                                                                                                                                                                                              /db_xref="taxon:10090"
/clone="J0738H04"
/clone_lib="Mouse two-cell stage embryo cDNA"
/dev_stage="two-cell stage embryo"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mouse two-cell stage embryo cDNA Mus musculus 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                        /organism-"Mus musculus"
/strain-"C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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/dev_stage="four-cell-embryo"
62 c 107 g 135 t
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0820C10"
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                                                                                                                                        66.7%;
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                                                                                                             0;
                                                                                                                                        Score 16;
Pred. No.
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Pred. No.
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1.1e+02;
hes 0;
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1.1e+02;
thes 0;
                                                                                                                                                               Length 439;
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VERSION
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AU045114/c
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                                               Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1810
Fax: 314 286 1810
                                                                                                                                                               White, Y., Wylie, T., Watersto
WashU-NCI human EST Project
                                                                                                                                                                           Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisel,G., Jost,S., Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B., White,Y., Wylie,T., Waterston,R. and Wilson,R.
                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                  AA682402
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Hirofumi Doi
Doi Bloasymmetry Project, ERATO
Japan Science and Technology Corporation (JST)
WBG Marive East 12F, 2-6 Nakase, Mihama-ku, Chiba 261-71, Japan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 451)

RO,M.S.H., Kitchen, J.R., Wang, X., Threat, T.A., Sun, T., DePalma, G.E., Liang, Y., Kargul, G.J., Sharara, R., Lim, M.K. and Doi, H. Systematic analyses of genes expressed in 16-cell mouse embryo (The
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Unpublished (1998)
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Location/Qualifiers
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{\tt est@watson.wustl.edu} lone is available royalty-free through LLNL ; contact the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mouse sixteen-cell 3', mRNA sequence.
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="J0930C10"
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/dev_stage="sixteen-cell-embryo"
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10 TTTATTTTGGGCTTCA 25
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                                                                                                                                                                                                                                                                                            High quality sequence stop: 427.
                                              Similarity
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Search completed: November 15, 2001, 06:39:15 Job time: 9291 sec

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160 161 162 163 164 165 166

156 157

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result

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Score

Match

Length

В

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SUMMARIES

AA251974

100.0 100.0 100.0

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AA251974 -67 bp mrNA EST 12-MAR-1997 zr64e01.sl Soares_NhHMPu_S1 Homo sapiens cDNA clone IMAGE:668184 3'similar to gb:D25272 !!!! ALU CLASS A WARNING ENTRY !!!! (HUMAN);,
                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 67)
          Elliston, K., Hawkins, M., Holme, Lennon, G., Marra, M., Parsons, Tan, F., Trevaskis, E., Waterst
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N23686 yw46a02.s1
N23691 yw46b01.s1
D82540 HUMHBC4284
N42962 yw53f06.s1
AI433008 th42e09.x
AA484085 ne73c10.s
H67529 yu68c11.s1
AQ553772 RPCI-11-4
AA528383 ne82h04.s
AF149534 AF149534
AI357151 gx62g10.x
AW574959 UI-HF-BNO
AI824649 wc48a05.x
AM574959 UI-HF-BNO
AI824649 wc48a05.x
AM573262 nm52d10.s
BF983677 602307244
AQ427220 CITBI-E1-
AA455670 aa22f08.s
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AA091710 m1216.seq
AA091710 m1216.seq
AA047496 oe19a05.s
AW082537 xb52e08.x
AA632600 np82c09.s
AA632600 np82c09.s
AA638816 ad41d11.s
AA68816 ad41d11.s
AA1306191 qw74f02.x
AA66208 qw74910.x
B95154 CIT-HSP-217
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H39321 DR20 IRNgam
AA828120 od71a01.s
AI864994 wk06cll.x
AA457423 a886b02.r
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AA228795 nc14e07.s
AA247810 hfe0642.s
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AW007890 wv46e10.x
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                Waterston
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AUTHORS
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similar to
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome S
Clone distribution: NCI-CGAP clone distribution I
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                           Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D.,
Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                            NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy
Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18;
                                                                                                                                                                  Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unpublished (1995)
Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The WashU-Merck EST Project
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           High quality sequence stop: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                            (bases 1 to 72)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note-*Organ: mixed (see below); Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (melanocyte 2NbHM, pregnant uterus NbHPU, and fetal heart NbHH19W) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 260232-265223, 340488-345479, and 484488-489479.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /tissue_type="Pooled human melanocyte, fetal heart,
pregnant uterus"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:668184"
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                                                                                                                                                                                                                                                                                                                                                                                                                                72 bp mRNA EST 09-MAR-2000 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2532618 contains Alu repetitive element;, mRNA sequence.
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Primates;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
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information
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SOURCE ORGANISM VERSION KEYWORDS

Homo sapiens

ACCESSION

mRNA sequence. AA251974 AA251974.1 GI:1887144

REFERENCE

AUTHORS

Hillier, L., Clark, N.,

ier,L., Clark,N., Dubuque,T.,
Hultman,M., Kucaba,T., Le,M.,
in,L., Rohlfing,T., Soares,M.,

RESULT 1 AA251974/c

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100.0 100.0 100.0 100.0

2 AA826076 20 AW769572 03 AI922803 AA346355

ALIGNMENTS

100

<u>8</u>8

AW082537 AA632600 AI305894

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100

AA017501 AA091710

AA847496

<u>6</u>6

100

228

BF983677 AQ427220

AA455670

AA730009

AA573262

AI696442

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122 122 126 126 128 133

AI357151 8 AW574959 2 AI824649

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105 107 107

145 159 159 157

100 100 100 100

AA247810

BF194862

AA228795 AA604960

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AA484085

AI433008

D82540

30 AQ553772 AA528383

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103

AI864984

AA828120

AA457423 AA835205

DEFINITION Locus

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REFERENCE
AUTHORS
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ORGANISM
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Best Local :
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                                                                                                                                                                                                                                                                      Source: IMAGE Consortium, LLNL This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hilller,L., Clark,N., Dubuque,T., Elliston,K., Hawkins,M., Holman,M., Hultman,M., Kucaba,T., Le,M., Lennon,G., Marra,M., Parsons,J., Rifkin,L., Rohlfing,T., Soares,M., Tan,F., Trevaskis,E., Waterston,R., Williamson,A., Wohldmann,P. and Wilson,R.

The WashU-Merck EST Project
                                                                                                                                                                                                                                             High quality sequence stop: 253
                                                                                                                                                                                                                                                                Seq primer: ml3 -40 forward
                                                                                                                                                                                                                                                                                                                                               Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                              Tel:
                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 75)
Hillier, L., Clark, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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YY80hll.sl Soares_multiple_sclerosis_2NbHMSP Homo sapiens cDNA

clone IMAGE:279909 3' similar to contains Alu repetitive eleme
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mRNA sequence.
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Insert Length: 508 Std Error: 0.00
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314 286 1810
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/tissue_type="multiple sclerosis lesions"
/dev_stage="Age 46"
/lab_host="DH10B (ampicillin resistant)"
/note="Vector: pT7T3D (Pharmacia) with a
                                                                                                                                                             /organism="Homo sapiens"
/db_xref="GDB:3898285"
                                                                                   /clone_lib="Soares_multiple_sclerosis_2NbHMSP"
/sex="male"
                                                                                                                         /db_xref="taxon:9606"
/clone="IMAGE:279909"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="Organ: stomach; Vector: pCMV-SPORT6; Site_1: Sall;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.69 kb. Life Technologies catalog #:
                                                                                                                                                                                                                            ocation/Qualifiers
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/db_xref="taxon:9606"
/clone="IndRGE:2532618"
/clone_lib="NCI_GGAP_Gas4"
/tissue_type="poorly differentiated adenocarcinoma with
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Pred. No. 2.2
0; Mismatches
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2.2;
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with a modified
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h 100.0%; Score 18; Similarity 100.0%; Pred. No. 18; Conservative 0; Mismatcl
                                                                                                                                                                                                                                                                                                                              Tel: 2016481008
Fax: 2016481007
Email: rhart@andromeda.rutgers.edu
sequence is similar to complement Cl inhibitor gene (M30688) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                                                                                                                                                                                                                         Seq primer: KS
                                                                                                                                                                                                                                                                                                      subcloned into PCRscript
                                                                                                                                                                                                                                                                                                                            contains alu element
                                                                                                                                                                                                                                                                                                                                                                                                                     Rutgers University
Dept of Biol Sci,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Identification of mRNAs regulated by interferon-gamma rat astrocytes by PCR differential display Neuroimmunomodulation 2, 347-355 (1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Contact: Hart RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kuchinke, W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             similar to complement C1 inhibitor, mRNA
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                                                                                                                     /Clone_lib="IFNgamma-induced astrocyte ESTs"
/note="cDNA from IFNgamma-induced cultured rat astrocytes
/mas screened by PCR differential display. Regulated cDNAs
were amplifed, sequenced and confirmed by dot-blots and
                                                                                               Northerns. * 25 c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /Clone="DR20"
                                                                                                                                                                                                        /strain="Sprague-Dawley"
/db_xref="taxon:10116"
                                                                                                                                                                                                                                        /organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       lesions from one patient was kindly provided G. Becker (NINDS/NIH). "
25 c 18 g 17 t
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; 1st strand cDNA was primed with a Not I - oligo(dT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hart, R.P. and Jonakait, G.M.
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Rodentia;
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Sciurognathi; Muridae; Murinae;
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               DB 158;
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                                              wk06cll.xl
similar to
             AI864984
AI864984.1
                                                                                AI864984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 801 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 84.
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Contact: Robert Strausberg, Ph.D.
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National Cancer Institute, Cancer Genome Anat
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                                                                                                                                                                                                                                                                                                                                                       /note="Vector: pAMP10; mRNA made from invasive ovarian tumor, cDNA made by oligo-dT priming. Non-directional cloned. Size-selected on agarose gel, average insert : 600 bp. Reference: Krizman et al. (1996) Cancer Resea
                                                                                                                                                                                                                                                                                                                               56:5380-5383.*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="ovary"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="IMAGE:1373352"
/clone_lib="NCI_CGAP_Ov2"
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                                                      90 bp mRNA EST 21-DEC-1999 NCI_CGAP_Lym12 Homo sapiens cDNA clone IMAGE:2411540 3'
                                          contains Alu repetitive element; , mRNA
               GI:5529091
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AA457423
IMAGE Consortium (info@image.linl.gov) for Seq primer: -28m13 rev1 ET from Amersham High quality sequence stop: 76.
                                                                                                                                                                                                   Schellenberg, K., Steptoe, M., T., Waterston, R. and Wilson, R. Washu-Merck EST project 1997 Unpublished (1997)
                                                                                                                                                                                                                                                                              1 (bases 1 to 95)
Hillier, L., Allen, M., Bowle
Kucaba, T., Lacy, M., Le, N.,
                                 This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                    Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                      4444 Forest Park Parkway,
                                                                                                                                                                                    Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                   EST
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aa86b02.r1
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Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
                                                                                                                                                             Washington University
                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleóstomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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DNA Sequencing by: Washington University Genome Clone distribution: NCI-CGAP clone distribution found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                              numan
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 195 Std Error: 0.00
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National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                 est@watson.wustl.edu
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/clone="IMAGE:2411540"
/clone_lib="NCI_CGAP_Lym12"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /tissue_type="lymphoma,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Stratagene fetal retina 937202 Homo sapiens cDNA clone 55 5' similar to contains Alu repetitive element;, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -40UP from Gibco.
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                                                                                                                                                                                                                                                       Bowles,L., Dubuque,T., Geisel,G., Jost,S., e,N., Lennon,G., Marra,M., Martin,J., Moore,B. eptoe,M., Tan,F., Theising,B., White,Y., Wylie
                                                                                                                                          School of Medicine way, Box 8501, St. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 18;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                        8501,
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                                                                                                                                      St.
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                                                                                                                                        Louis, MO 63108
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RESULT 8
AA835205/c
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AUTHORS
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KEYWORDS
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Best Local
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                                                                                                                                                                                                                                                                                                                          Email: est@watson.wustl.edu
This clone is available royalty-free through LLNL;
IMAGE Consortium (info@image.llnl.gov) for further j
Seq primer: -40ml3 fwd. ET from Amersham.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ak64h01.s1 Barstead pancreas HPLRB1 Homo sapiens cDNA clone IMAGE:1412689 3' similar to contains alu repetitive element; contains element KBR repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              White,Y., Wylie,T., Watersto
WashU-NCI human EST Project
Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hillier, L., Allen, M., Bowles, L., Dubuque, T., Geisel, G., Jost, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Krizman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin,
J., Moore,B., Schellenberg,K., Steptoe,M., Tan,F., Theising,B.,
White,Y., Wylle,T., Waterston,R. and Wilson,R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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314 286 1810
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              [AATTCGGATCCTTG], digested with Not I and Eco RI sites of the modif Library constructed by Bob Barstead.
                                                                                                                                        with a modified
                                                                                                                                                                                                                                              /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1412689"
                                                                                                               /note="Organ: pancreas; Vector: pT7T3D-Pac (Pharmacia)
with a modified polylinker; Site_1: EcoRI; Site_2: Not
lst strand cDNA was primed with a Not I - oligo(dT) pr
                                                                          dev_stage="adult, 34 years"
/lab_host="DH10B"
                                                                                                                                                                                                                  sex="female"
                                                                                                                                                                                                                              /clone_lib="Barstead pancreas HPLRB1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host="SOLR (kanamycin resistant)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="Stratagene fetal retina 937202"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="IMAGE:838155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ∕organism="Homo sapiens"
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                                     double-stranded cDNA was ligated to Eco RI adaptors CGATCCTTG], digested with Not I and cloned into the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        mRNA
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                     the modified pT7T3 vector
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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                                                                                                                 oligo(dT) primer
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BASE COUNT
ORIGIN
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AUTHORS
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ORGANISM
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ORIGIN
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                       source
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ggcggagcttgcagtgag 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: David B. Krizman, Ph.D.
cDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 757 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Insert Length: 757 Std Error: 0.00
Seq primer: -40m13 fwd. ET from Amersham
High quality sequence stop: 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Onpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AA604960 102 bp mRNA EST 08-OCT-199/
no93b10.s1 NCI_CGAP_Pr2 Homo sapiens cDNA clone IMAGE:1114363
similar to contains Alu repetitive element;contains element M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cgapbs-r@mail.nih.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
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1 (bases 1 to 102)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                   14
                                            /dev_stage="45 years old"
//dev_stage="45 years old"
//lab_host="DH10B"
//note="Vector: pAMP10; Site_1: Not1; Site_2: EcoRI; Ist
strand cDNA was primed with oligo(dT)17 on 50 ng of
DNAse-treated, total cellular RNA obtained from 5,000-10
,000 microdissected preneoplastic cells
histologically-determined to be prostatic intraepithelial
neoplasia 2 (PIN2) cells. Double-stranded cDNA was
ligated to EcoRI adaptors, 5 cycles of PCR applied to the
cDNA with an adaptor-specific primer, and the resulting
PCR product subcloned into pAMP10 by the UDG-cloning
method (Life Technologies). Average insert size is 600
bp. NOTE: Not directionally cloned. This library was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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               constructed by 1
                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1114363"
/clone_1ib="NCI_CGAP_Pr2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    /sex="Male"
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Pred. No.
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                                 David Krizman.*
             g
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Query Match Best Local

18;

Conservative

Similarity

100.0%; S 100.0%; F tive 0;

Pred. No. 2

DB 9; 2.2;

Length 102;

Indels.

0;

Gaps

0;

Mismatches

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RESULT 11
AA247810/c
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AA228795/c
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AA247810
hfe0642.seq.F |
cDNA 5', mRNA
                                                                                                                                                                                                                                                                                                                                l Similarity
18; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cDNA Library Preparation: David B. Krizman, Ph.D. CDNA Library Arrayed by: Genome Systems Inc., Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Cente Clone distribution: NCI-CGAP clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AA228795 103 bp mRNA EST 20-AUG-1797, ncl4e07.sl NCI_CGAP_Prl Homo sapiens cDNA clone IMAGE:1008132 similar to contains Alu repetitive element;contains element MER28 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           www-bio.llnl.gov/bbrp/image/image.html
Seq primer: -41m13 fwd. ET from Amersh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tissue Procurement: W. Marston Linehan, M.D., Rodrigo Chuaqui, M.D., Michael Emmert-Buck, M.D., Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      High quality sequence stop: 81.
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National Cancer Institute, Cancer Genome Anat
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1 (bases 1 to 103)
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Mammaila; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  strand cDNA was primed with oligo(dT)17 on 50 ng of DNAse-treated, total cellular RNA obtained from 5,000-10,000 microdissected, histologically normal prostate epithelial cells. Double-stranded cDNA was ligated to EcoRI adaptors, 5 cycles of PCR applied to the cDNA with an adaptor-specific primer, and the resulting PCR product subcloned into pAMP10 by the UDG-cloning method (Life Technologies). Average insert size is 600 bp. NOTE: Not directionally closed with the contract co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    directionally cloned. David Krizman. "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /dev_stage="45 years old"
/lab_host="DH10B"
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/db_xref="taxon:9606"
/clone="IMAGE:1008132"
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Human fetal heart,
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7089e07.x1
similar to
Tissue Procurement: Christopher Moskaluk, M.D., Emmert-Buck, M.D., Ph.D.
                                                                 Tumor Gene Index
Unpublished (1997)
                                                                                                                                                                                                                     BF194862.1
EST.
                               Email: cgapbs-r@mail.nih.gov
                                              Contact: Robert Strausberg, Ph.D.
                                                                                           NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anat
                                                                                                                                                                 Eukaryota; Metazoa;
                                                                                                                                                                                   Homo sapiens
                                                                                                                                                                                                                                                      BF194862
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                                                                                                                                                Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BACKWARD: 5' CCAGTGAATTGTAATACGACTCACTATAGGGCG
Seq primer: 5' GAAATTAACCCTCACTAAAGGG 3'.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Liew
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Department of Laboratory Medicine and Pathobiology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cDNAs from human
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Mammalia; Eutheria;
1 (bases 1 to 105)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 adaptor primer. ECOK1 adaptor digestion with XhoI, for direct predigested lambda ZAP Express.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Clone_lib="Human fetal heart, Lambda ZAP Express"
/lab_host="E. coli XLI-Blue"
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
/note="Vector: Lambda ZAP Express; Site_1: EcoRI; Site_2:
XhoI; mRNA was purified from human fetal hearts (8-10
weeks). cDNA was synthesized using a XhoI-Oligo dT
adaptor-primer. EcoRI adaptors were ligated, followed by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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                                                                                                                                                                                                                                                                repetitive element;,
                                                                                                                                                                                                                                                                                                    mRNA
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                                                                                              Project (CGAP),
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IMAGE:3643500 3'
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               Michael
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cDNA Library Preparation: M. Bento Soares, Ph.D. cDNA Library Arrayed by: Greg Lennon, Ph.D. DNA Sequencing by: Washington University Genome Sequencing Center Clone distribution: MCI-CGAP clone distribution information can be

Consortium/LLNL, send

email to:

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SOURCE
ORGANISM
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Hiller,L., Lennon,G., Becker,M., Bonaldo,M.F., Chiapelli,B., Chissoe,S., Dietrich,N., DuBuque,T., Favello,A., Gish,W., Hawkins,M., Hultman,M., Kucaba,T., Lacy,M., Le,M., Le,N., Mardis,E., Moore,B., Morris,M., Parsons,J., Prange,C., Rifkin,L., Rohlfing,T., Schellenberg,K., Soares,M.B., Tan,F., Thierry-Meg,J., Trevaskis,E., Underwood,K., Wohldmann,P., Waterston,R., Wilson,R. and Marra,M. Generation and analysis of 280,000 human expressed sequence tags Genome Res. 6 (9), 807-828 (1996)
                                                                                                                                                                             Seq primer: m13 -40 forward High quality sequence stop: 313.
                                                                                                                                                                                                                      Source: IMAGE Consortium, LLNL free through LLNL; contact the This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
                                                                                                                                                                                                                                                                                                                                                                     Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N23686 107 bp mRNA EST 28-DEC-1995
yw46a02.sl Weizmann Olfactory Epithelium Homo sapiens cDNA clone
IMAGE:255242 3' similar to contains Alu repetitive element;contains
element MER5 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                     Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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: 314 286 1810
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/organism-"Homo sapiens"
/db_xref-"GDB:3865651"
/db_xref-"taxon:9666"
/clone-"IMAGE:255242"
/clone_11b-"Weizmann Olfactory Epithelium"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1500552-1502855). Subtraction by Bento Soares and M. Fatima Bonaldo. * 19 c 31 g 26 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Note-*Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: ECO RI; Plasmid DNA from the normalized library NCI_CGAP_Kid3 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library cloneIDs 1322376-1323911, 1456007-1456775, and
                                                                                                                                                         Location/Qualifiers
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/clone_lib="NCI_CGAP_Kidll"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Chissoe, S., Dietrich, N., DuBuque, T., Favello, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M.B., Tan, F., Thierry-Meg, J., Trevaskis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M. Generation and analysis of 280,000 human expressed sequence tags
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IMAGE Consortium (info@image.linl.gov)
Seq primer: m13 -40 forward
High quality sequence stop: 342.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: esteracountium, LLNL
Source: IMAGE Consortium, LLNL
This clone is available royalty-free through LLNL;
This clone is available royalty-free through LLNL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800
Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hillier, L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          yw46b01.s1 Weizmann Olfactory Epithelium Homo sapiens cDNA clone IMAGE:255241 3' similar to contains Alu repetitive element;contains element MER5 repetitive element; mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Genome Res. 6 (9), 807-828 (1996)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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/sex="Pemale"
/tissue_type="olfactory epithelium"
/tissue_type="olfactory epithelium"
/dev_stage="35 year old"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: nose; Vector: pBluescript SK:, Site_1: EcoRI
/note="Organ: nose; Vector: pBluescript SK: Site_1: EcoRI
/site_2: XhoI; Cloned unidirectionally. Primer: Oligo
dT Olfactory epithelium, normal. Average insert size: 0.8
kb: Uni-ZAP XR Vector. Library constructed by N. Walker,
kb: Uni-XAP XR Vector. Tibrary constructed by N. Walker,
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/note="Organ: nose; Vector: pBluescript SK:, Site_1: EcoF.
/note="Organ: nose; Vector: pBluescript SK:, Site_1: EcoF.
/note="Organ: nose; Vector: pluescript Sk:, Site_1: EcoF.
/note="Organ: nose; Vector: Organization of State Size: 0."
/note="Organization of Size: 0."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/db_xref="GDB:3865650"
/db_xref="taxon:9606"
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/dev_stage="35 year old"
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Pred. No. 2
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TITLE
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D82540
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ORIGIN
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ORGANISM
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ORIGIN
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Best Local Similarity 100.

Matches 18; Conservative
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Best Local Similarity 100
Matches 18; Conservative
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                                                                              29 GGCGGAGCTTGCAGTGAG 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         Institute for Molecular and Cellular Regulation, Gunma University 3-39-15 Showa-machi, Maebashi Gunma 371, Japan Tel: 272-20-8856
Fax: 272-20-8896
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human pancreatic islet ESTs
Unpublished (1995)
Contact: Jun Takeda
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 110)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Takeda, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               D82540.1 GI:1183498
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                                                                                                                                                                                                                                                                                                                                                                                                                   jtakeda@sb.gunma-u.ac.jp.
Location/Qualifiers
                                                                                                                                                                                                                                     /clone_lib="Rhuman pancreatic islet"
/clone_lib="Rhuman pancreatic islet"
/clone="Yector: Lambda ZAPII; Site_1: Eco RI; Site_2: Xho
I; mRNA was prepared from normal adult human islets. cDNA
was directionally synthesized from the Xho I in the vector
to the EcoRI site. cDNA was size fractionated to remove
sequences <1000 bp in size."
sequences <1000 bp in size."
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41 c 24 g 22 t 4 others
                                                                                                                                                                                                                                                                                                                                                                       organism="Homo sapiens"
db_xref="taxon:9606"
                                                                                                                                          100.0%; Sc.
/ 100.0%; Pr
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100.0%; Pred. No. 2.2;
httve 0; Mismatches 0;
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Pred. No. 2.2;
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Maximum DB seq length: 2000000000
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219.877 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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18	18	18	18	18	18	Score	
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93	5 C1	93	97	97	97		
HSU02050	HSA248384	HSU02063	HUMALCE22	HUMALCE44	HUMALCE162	ID	SUMMARIES
U02049 Human clone U02050 Human clone	AJ248384 Homo sapi	U02063 Human clone	M87926 Human carci	M87927 Human carci	M87924 Human carci	Description	

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Query Match
Best Local Similarity 100.0%; 19 Matches 18; Conservative 0;
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1 (bases 1 to 107)
Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model of post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
                                                                                                                                                                                                                                                                                                                                                                                                                 HUMALCE162 107 bp ss-RNA PRI 15-APR-1994
                                                                                                                                                                                                                                                                                                                                                      Homo sapiens male embryo carcinoma cDNA to other RNA.
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/dev_stage="embryo"
/sex="male"
                                                                                             /tissue_type="carcinoma"
30 c 35 g 1
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PTU14709
HS73F11R
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         0;
                                   Length 107;
         Indels
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U67818 Human prima
261176 H.sapiens C
X55932 Human DNA f
U18390 Human Alu s
U67831 Human prima
U67827 Human prima
AL162993 H.sapiens
I51997 Sequence 5
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Z62833 H.sapiens C
U18388 Human Alu s
X55933 Human DNA f
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$70694 (repetitive
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U14568 ***ALU WARN
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X75335 H.sapiens A
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U14705 Human Alu-S
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Y08944 H.sapiens
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      Gaps
      0;
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HUMALCE44
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            post-transcriptional selection of master sequences J. Mol. Biol. (1992) In press Location/Qualifiers
                                                                                                                                                                                             post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                      Homo sapiens male embryo carcinoma cDNA to other RNA Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                              Human carcinoma cell-derived Alu RNA transcript, clone CE22.
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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M87927.1 GI:174877
      Similarity
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39 c 44 g 2
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/sex="male"
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Pred. No. 0.79;
Mismatches
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                 Length 135;
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REFERENCE AUTHORS TITLE

SOURCE ORGANISM

Homo sapiens Alu repeat

VERSION ACCESSION KEYWORDS

M87924.1 GI:174871

LOCUS DEFINITION RESULT 1 HUMALCE162

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HS178H6F/c
                                                                                                                                                                                                        ACCESSION
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                                                                                                                                                                                                Human clone 4 Alu
U02063
                                                                                                                                                                                                                                                                                                                                                                               18;
                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
1 (bases 1 to 234)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Clones are available from the UK MRC Human Genome Mapping Project Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL: http://www.bgmp.mrc.ac.uk/ for details or contact: biohelp@hgmp.mrc.ac.uk.
                                             methylation
                                                                                                                                                                                       002063.1
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Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire,
CB10 1RQ, England. E-mail contact: humquery@sanger.ac.uk
                                                  Alu transcripts: cytoplasmic localisation and regulation by DNA
                                                                      Liu, W.M., Maraia, R.J., Rubin, C.M. and Schmid, C.W.
                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 (bases 1 to 224)
Cross,S.H., Charlton,J.A., Nan,X.
Purification of CpG islands using
Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 224)

Dodsworth, S.J., Huckle, E., Wilkinson, P. and Micklem, G.
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CpG island; genomic Msel fragment.
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H.sapiens CpG island DNA genomic Msel fragment,
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                           eic Acids Res.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /dev_stage="adult"
/tissue_type="blood"
/clone_lib="CGI-1"
/clone="178h6"
a 61 c 55 g
                                                                                                                                                                                      GI:406898
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
/db_xref="taxon:9606"
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Pred. No. 0.7
0; Mismatches
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                                                                                                                      Euteleostomi;
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BASE COUNT 56
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                                                                                                                                                                                                                                                                                                                                                       Animal Genetics, N.I.Vavilov Institute of General Genetics RAS, Gubkin Str. 3, Moscow B-333, 117809 GSP-1, RUSSIA The STS markers registered were developed to clones from Notl library of human chromosome 3 received by E.R. Zaharoveku, /vacciliation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens STS NRL-402R, AJ248384
                                                                                                                                                                                                                                                      Institute of the Russian Academy of Sciences. The Noti clones were used to construct Noti map of human chromosome 3 by FISH and mapping by a somatic cell hybrid panel.
                                                                                                                                                                                                                                                                                                                 3 received by E.R. Zabarovsky (Karolinska
Institute, Sweden) as a result of collaborative
research work with Engelhardt Molecular Biology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sulimova,G.E., Odina,I.G., Kunizheva,S.S. and Kompaniitzev,A.A. Creating NotI-STS Markers for Human Chromosome 3 Mol. Biol. 33, 698-703 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (23-SEP-1993) University of and Cellular Biology, Davis, CA 95616 Location/Qualifiers
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STS.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Liu,W.M.
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Similarity 100.0%;
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                                    22. .215
/standard_name="NRL-402R"
/note="STS PCR product"
                                               /PCR_conditions="95deg.
1.0min"
                                                              /note="NRL-402R forward primer"
/PCR_conditions="95deg. 0.8min,
                                                                                                                                /map="3p21.3"
                                                                                                                                              /cell_type="mouse/human microcell
/cell_line="MCH903.1"
                                                                                                                                                                             /chromosome=*3"
                                                                                                                                                                                           /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                             clone_lib="NotI-linking library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /cell_line="HeLa"
/cell_type="epithelial cell"
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/db_xref="taxon:9606"
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            Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                        HSU02050 240 bp
Human clone AZA7 Alu
                                                                                                                                                                                                                                                                                                                                                                                     Submitted (23-SEP-1993) Liu W.M., Molecular and Cellular Biology, D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; 1 (bases 1 to 236)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    methylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Liu, W.M., Marala, R.J., Rubin, C.M. and Schmid, C.W. Alu transcripts: cytoplasmic localisation and regulation by DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      U02049.1 GI:406884
                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
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   (bases 1 to 240)
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                                                                      GI:406885
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Location/Qualifiers
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/note="NRL-402R reverse
/PCR_conditions="95deg.
1.0min"
                                                                                                                                                                                                                                                                                           cell_type="epithelial cell"
                                                                                                                                                                                                                                                                                                                   /sex-"female"
                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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            Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                  ., University of California, Davis, Davis, CA 95616 USA
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                                                                                                                                                                                                                                                                               Submitted (13-NOV-1997) Pediatry, University of Montreal, Sainte-Justine Hospital, Research Center (Charles Bruneau Center of Cancerology), 3175 Cote Sainte-Catherine, Montreal, Quebec H3T-1C5,
                                                                                                                                                                                                                                                                                                                                                2 (bases 1 to 244)
Zietkiewicz, E., Richer, C.
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Zietkiewicz,E., Richer,C
Phylogenetic affinities
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AF034649
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Tarsii; Tarsiidae; Tarsius.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Liu, W.M.
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            /rpt_family="tarsier Alu"
/rpt_type=dispersed
69 c 78 g 37
                                                                                     /organism="Tarsius syrichta"
/db_xref="taxon:9478"
/clone="TARS25"
                                                                     'note="PCR-amplified"
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/db_xref="taxon:9606"
/clone="AZA7"
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 Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 248)
                                       Homo sapiens
                                                                                          Homo sapiens clone 18ptelc6.59t3 sequence. AF270578
                                                                                AF270578.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (18-OCT-1996) J. Gu, University Of North Carolina-Chapel Hill, Pharmacology, 1106 Flob Cb7365, North Carolina 27599, USA Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gu,J.J., Spychala,J. and Mitchell,B.S.
Regulation of the human inosine monophosphate dehydrogenase type gene. Utilization of alternative promoters
J. Biol. Chem. 272 (7), 4458-4466 (1997)
97172526
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/map="q31.3-q32"
/clone="phage 1111a"
/dev_stage="adult"
                                                                                                                                                                                                                                                                                                                   /note="P1"
                                                                                                                                                                                                                                                                                                                        /gene="inosine monophosphate dehydrogenase type I
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/db_xref="taxon:9606"
/chromosome="7"
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260686.1 GI:10327an
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M87925.1 GI:174872
Alu repeat
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Sinnett,D., Richer,C., Deragon,J.-M. and Labuda,D.
Alu RNA transcripts in human embryonal carcinoma cells. Model post-transcriptional selection of master sequences
J. Mol. Biol. (1992) In press
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Riethman, H.C. and Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Riethman,H.C. and Moyzis,R.K. Integration of telomeric DNA sequences with the human \,
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/db_xref="taxon:9606"
/cell_line="NTera2D1"
                                                                                                                                                                                                                                                                                /tissue_type="carcinoma"
66 c 80 g 37 t
                                                                                                                                                                                                                                                                                                                /dev_stage="embryo"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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74 c 55 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /map="18ptel"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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                                                                                                                                                                                                        Score 18; DB 97;
Pred. No. 0.72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 18; DB 89
Pred. No. 0.72;
                                                             DNA
                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Alu
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                                                             PRI
                                                                                                                                                                                                                       Length 249;
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clone CE21.
                                                             19-OCT-1995
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DNA

genomic

Msel fragment,

clone 31b4, forward

10 ul

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Mismatches

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PRI

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Length 262; Indels

30-100 ng

Perkin Elmer

TC

72 35

degrees C for 1.00 minute(s)

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AUTHORS
TITLE
JOURNAL
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                                                                        Primer B: TCA
STS size: 81
PCR Profile:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18;
                                                                                                                                     Email: pieter@dejong.med.buffalo.edu
Primer A: TTATTCTTAAGGGAAGAGGTTC
                                                                                                                                                                          Human Genetics Department
Roswell Park Cancer Institute
Elm and Carlton Streets, Buffalo,
Tel: 716-845-3168
Fax: 716-845-8449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             G38317 262 bp
RPCI-4-790D12T7 Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (16-OCT-1995) The Sanger Centre, Hinxton, Cambridgeshire, CB10 IRQ, England. E-mail contact: humquery@sanger.ac.uk
2 (bases 1 to 257)
Cross,S.H., Charlton,J.A., Nan,X. and Bird,A.P.
Purification of CpG islands using a methylated DNA binding column Nat. Genet. 6 (3), 236-244 (1994)
                                                                                                                                                                                                                                                                              Contact: Pieter J. de Jong
                                                                                                                                                                                                                                                                                                                          Unpublished (1998)
                                                                                                                                                                                                                                                                                                                                                                    de Jong, P.J.
                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    G38317.1
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Clones are available from the UK MRC Human Genome Mapping Project
Resource Centre, Hinxton, Cambridgeshire CB10 1RQ, UK. See URL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      http://www.hgmp.mrc.ac.uk/ for details
or contact: biohelp@hgmp.mrc.ac.uk.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94282070
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1 (Dases 1 to 257)

MacDonald, M., Huckle, E., Wilkinson, P. and Micklem, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Direct Submission
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human.
                                                                                                                                                                                                                                                                                                                                                                                          (bases
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                              Denaturation
                                                  Presoak:
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/clone_lib="CGI-1"
/clone="31b4"
                                                                                                                                                                                                                                                                                                                                                                                     1 to 262)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
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Primates;
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degrees C :
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    for
for
r 0.00 minute(s)
r 30 second(s)
r 30 second(s)
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BASE COUNT
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AUTHORS
TITLE
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Best Local :
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                                                                                                                                           primer_bind
repeat_region
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                                                                                                                                                                                                                                                                                   Direct Submission

Submitted (15-SEP-1994) Wojciech Makalowski, National Center for Submitted (1
                                                                                                                                                                                                                                                                                                                                                                                                                                                A young Alu subfamily amplified independently in human and African great apes lineages.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human Alu-Sb2 repeat, U14706
                                                                                                                                                                                                                                                                                                                                                                            Makalowski,W.
                                                                                                                                                                                                                                                                                                                                                                                                                      95140622
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 262)
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                     62
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Primer:
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KCL:
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             complement(244..26
69 c 89 g
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68. .89
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                                                      /rpt_type-tandem
/evidence-experimental
/rpt_family-"Alu-Sb2"
/rpt_unit=1..262
                                                                                                                                              <1. .>262
                                                                                                                                                                                                      /organism="Homo sapiens"
/db_xref="taxon:9606"
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/db_xref="taxon:9606"
/clone_lib="Human"
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clone HUM-10.
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Pred. No. 0.72;
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Succes

DB 97; 3.72; es 0;	Search completed: November 15, 2001, 06:17:28 Job time: 8013 sec	Oy 1 ggcggagcttgcagtgag 18	Matches 18; Conservative 0; Mismatches 0; Indels	Query Match 100.0%; Score 18; DB 97; Length 262; Best Local Similarity 100.0%; pred No 0 72.
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Database :
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

C 87654321	Result
18 18 18 18 18 17 17	Score
100 0 196848 75.0 49306 75.0 63031 75.0 161492 75.0 170264 75.0 202915 70.8 141292 70.8 165633	Query Match Length DB
86 88 77 64 88 72 78	
AC007684 AC022237 AC087465 AC016693 AC024589 AC060773 AF235106 AC006924	SUMMARIES
AC007684 Homo sapi AC022237 Homo sapi AC087465 Homo sapi AC087693 Homo sapi AC024589 Homo sapi AC060773 Homo sapi AF235106 Homo sapi AC006924 Homo sapi	Description

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AC007684 196848 bp DNA Homo sapiens BAC clone RP11-449G16 from 2, complete sequence. AC007684 AC007684.3 GI:5836173 HTG. human. HOmo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 196848) Sulston, J. E. and Waterston, R. Toward a complete human genome sequence Genome Res. 8 (11), 1097-1108 (1998) 97053792 2 (bases 1 to 196848) Edwards, J., Wohldmann, P., Hawkins, M. and Harkins, R. The sequence of Homo sapiens BAC clone RP11-449G16 3 (bases 1 to 196848) Waterston, R. H. Direct Submission Submitted (29-MAY-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. Louis Mo 63108, USA 4 (bases 1 to 196848) Waterston, R. H. Direct Submission Submitted (08-SEP-1999) Genome Sequencing Center, Washington Submitted (08-SEP-1999) Genome Sequencing Center (08-SEP-1999) Genome Sequencing Center (08-SEP-1999) Genome Sequencing Center (08-SEP-1999) Genome Sequenci	ALIGNMENTS	17 70.8 239254 76 AC079569 ACC79569 Mus muscu 16 66.7 1233 8 TRCWPWH 16 66.7 1233 8 AB017819 AB017819 Theragra ch 16 66.7 3923 8 AB017819 AB017819 Theragra ch 16 66.7 13923 8 AB017819 AB017819 Theragra ch 16 66.7 11199 1 AE001138 AE001138 Borrelia 16 66.7 23091 65 AC017994 AC015965 Drosophil 16 66.7 38261 85 AC000038 AC0015965 Drosophil 16 66.7 38261 85 AC000038 AC001596 AC001799 AC017994 Drosophil 16 66.7 110302 83 AP002013 16 66.7 112474 60 AC007150 AC0007150 Drosophil 16 66.7 114644 83 AP002083 16 66.7 154090 88 AC025577 AC024351 AC002574 Homo sapi 16 66.7 154090 88 AC025577 AC02579 AC02579 Homo sapi 16 66.7 156150 69 AC025577 AC025862 AC00358 AC003584 AC0035862 AC003584 AC003584 AC003584 AC003584 AC003584 AC005579 AC05682 AC005682 AC005
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AUTHORS
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                                                                                                                                                                    Direct Submission
Submitted (21-DEC-1999) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Sep 8, 1999 this sequence version replaced gi:5001493.
                                                                                                                                                                                                                                                                               Waterston, R.
                                                                                                                                                                                                                                                                                                    MO 63108, USA
5 (bases 1 to 196848)
Center project name: H_NH0449G16
                    Web site: http://genome.wustl.edu/gsc
Contact: sapiens@watson.wustl.edu
------ Summary Statistics
                                                                                                   Center: Washington University Genome Sequencing Center Center code: WUGSC
                                                                                                                                                  - Genome Center
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clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions. NOTICE: This sequence may not represent the entire insert of this

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:
Mapping information for this clone was provided by Dr. John D.
Mapping, Department of Genetics, Washington University, St. Louis
MCD. For additional information about the map position of this
sequence, see http://genome.wustl.edu/gsc

SOURCE INFORMATION:

The RPCI-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tateno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (http://www.resgen.com) or Pieter de Jong and coworkers at the Roswell Park Cancer Institute (http://bacpac.med.buffalo.edu)
VECTOR: pBACe3.6

NEIGHBORING SEQUENCE INFORMATION:
The clone sequenced to the left is RP11-395B14. Actual start of this clone is at base position 1 of RP11-449C16; actual end is at base position 196848 of RP11-449G16.

ATURES repeat_region repeat_region repeat_region repeat_region repeat_region repeat_region source repeat_region repeat_region /rpt_family="(TG)n" 357. .423 /rpt_family-"L1" 456. .746 /rpt_family="Alu" 286. .319 /rpt_family="L1" 747. .1036 /rpt_family="L1" 320. .356 /chromosome="2" /map="2" 1. .196848 /clone="RP11-449G16" /clone_lib="RPCI-11" /organism="Homo sapiens" /db_xref="taxon:9606" /rpt_family="L1" /rpt_family="L1" Location/Qualifiers rpt_family="Alu" . 1882

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Direct Submission
Submitted (15-DEC-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                        3 (bases 1 to 49306)
Abola,A.P., Bruno,D., Conn,L., Dela Rosa,M., Faulkner,D.,
Federspiel,N., Glukhov,S., Hansen,N., Herman,Z.S., Hyman,R.,
Lam,B., Mao,J., Marathe,R., Miranda,M., Morehouse,A.J., Nguyen,M.,
Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J.,
Yu,S. and Davis,R.W.
                                                                                                                                                              Direct Submission
Submitted (27-JAN-2000) DNA Sequencing and Technology Center,
Stanford University, 855 California Avenue, Palo Alto, CA 94304,
                                                                                                                                                                                                          2 (bases 1 to 49306)
Bruno,D., Conn,L., Dela Rosa,M., Federspiel,N., Foreman,P., Glukhov,S., Hansen,N., Hyman,R., Mao,J., Marathe,R., Morehouse,A.J., Oefner,P., Palm,C.J., Ramirez,D., Wilhelmy,Vu,S. and Davis,R.W.
                                                                                                                                                                                                                                                                                           Mao,J., Lam,B., Marathe,R., Miranda,M., Herman,Z.S., Hyman,R., Oefner,P., Palm,C.J., Ramirez,D., Southwick,A.M., Wilhelmy,J., Yu,S. and Davis,R.W. Unpublished
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clone RP11-323C17 T7
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                                                                                                                                                                                                                              Ramirez, D., Wilhelmy, J.,
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COMMENT

On Dec 15, 2000 this sequence version replaced gi:11095463

COMMENT

TITLE

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ORGANISM
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JOURNAL
                                                                                                                                                                                                                                                                                                                                AUTHORS
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Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, S., Barran, B., Bastlen, V., Boguslawkiy, L., Boukhgalter, B., Brown, A., Camarotata, J., Campopiano, A., Choepel, Y., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Diaz, J.S., Dodge, S., Faro, S., Ferreira, P., FitzHugh, W., Gage, D., Galagan, J., Gardyn, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Gardyn, S., Ginde, S., Goyette, M., Lamazares, R., Landers, T., Johnson, R., Jones, C., Karatas, A., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Levine, R., Liu, G., MacLean, C., Macdonald, P., Marquis, N., Matthews, C., McCarthy, M., McEwan, P., McRernan, K., Murphy, T., Naylor, J., Meneus, L., Mihova, T., Mienga, V., Murphy, T., Naylor, J., Nguyen, C., Norbu, C., Norman, C.H., Phunkhang, P., Pierre, N., Pollara, V., Raymond, C., Retta, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 cagatttattttgggctt 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This sequence was finished as follows unless otherwise noted: all regions were double stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence
                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Prinates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 63031)
Birren,B., Linton,L., Nusbaum,C. and Lander,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HTG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE SAMPLING
AC087465
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens chromosome
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                                                                                                                                                                                                                                                                                                                                                                           Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens chromosome 15, clone RP11-94P14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      16374 a
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Center clone name: RP11-323C17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /clone_lib="RPCI human BAC library 11"
8614 c 8562 g 15756 t
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Pred. No.
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15 clone RP11-94P14 map 15,
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Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (05-JAN-2001) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Apr 12, 2001 this sequence version replaced gi:12039478.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rieback, M., Riley, R., Rise, C., Rogov, P., Roman, J., Rosett
Roy, A., Santos, R., Schauer, S., Schupback, R., Seaman, S., Sougnez, C., Spencer, B., Stange-Thomann, N., Stojanovic, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wilson, B., Wu, X., Wyman, D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strauss, N., Subramanian, A., Talamas, J., Tesfaye, S., Theodore, J., Traves, M., Travis, N., Trigilio, J., Vassiliev, H., Viel, R., Vo, A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zembek,L., Zimmer,A. and Zody,M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             overlap relationships among clones to be deduced. However, it should not be assumed that this clone will be sequenced to completion. In the event that
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NOTE: This record contains 76 individual sequencing reads that have not been assembled into contigs. Runs of N are used to separate the reads and the order in which they appear is completely arbitrary. Low-pass sequence sampling is useful for identifying clones that may be gene-rich and allows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       be preserved.
                                                                                                                                                              10660 10759: gap of 100 bp
10760 11477: contig of 718 bp
11478 11577: gap of 100 bp
11578 12297: contig of 720 bp
12298 12397: gap of 100 bp
12398 13126: contig of 729 bp
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Center clone name: 94_P_14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Web site: http://www-seq.wi.mit.edu
14063 14802: contig of 740 bp in length
14803 14902: gap of 100 bp
14903 15649: contig of 747 bp in length
15650 15749: gap of 100 bp
15750 16484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 720 819: gap of
820 1577: cont
1578 1677: gap of
1678 2431: cont
2432 2531: gap of
                                                                                                                        13127 13226: gap of 100 1
13227 13962: contig of 736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100 bp
183 3382: contig of 751 b
183 3382: gap of 100 bp
83 4099: contig of 717 hr
30 4199: gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100 bp 1 length 107 bp 1 length 15768: gap of 112 bp in length 6478: contin
                                                                                                                                                                                                                                                                                                                                           8982: contig of
9082: gap of 10
9832: contig of
                                                                                                                                                                                                                                                                                                                                                                                                        6578: gap of 100 bp
7284: contig of 706 bp in length
7384: gap of 100 bp
8133: contig of 749 bp in length
8233: gap of 100 bp
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                                                                                                                                                                                                                                                                                           or 100 bp
contig of 727 b
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contig of 754 bp in length
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contig of 717 bp
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16456: contig of

in length

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8870 38969:
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                           43838: gap of 100 bp 44578: contig of 740 bp in length 44678: gap of 100 bp 45432: contig of 754 bp in length 45532: gap of 100 bp 46269: contig of 737 bp in length
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27234: contig of
27334: gap of
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20628: contig of 713 b
0728: gap of 100 bp
21435: contig of 707 b
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38043: contig of 699 bp in length
143: gap of 100 bp
38869: contig of 726 bp in length
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36415: contig of 755 bp
315: gap of 100 bp
37244: contig of 729 bp
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34724: contig of 748 bp
324: gap of 100 bp
35560: contig of 736 bp
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33063: contig of 746 bp
163: gap of 100 bp
33876: contig of 713 bp
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17307: contig of
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28884: contig of 733 bp in length
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100 bp in length
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23898: contig of 737 bp in length
98: gap of 100 bp
24746: contig of 748 bp in length
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96: contig of
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6: contig of 725 bp in length
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51: contig of 701
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15: contig of 706
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contig of 580 bp
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contig of 730 bp
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TITLE
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Best Local
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Chemistry: Dye-terminator Big Dye; 22% of reads
Assembly program: Phrap; version 0.990319
                                                                                                                                                                                                                                                                                               Submitted (04-DEC-1999) Genome Sequencing Center, Washington University School of Medicine, 4444 Forest Park Parkway, St. MO 63108, USA
On Mar 13, 2000 this sequence version replaced g1:6838893.
                                                                                                Sequencing vector: M13; 78%
Sequencing vector: plasmid; 22%
    Consensus quality:
                                                                                                                                                               Center project name: H_NH0094P14
                                                                                                                                                                                                                         Center: Washington University
Center code: WUGSC
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Waterston, R.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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18; Conserv
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51397 52108: contig of 712 bp in length

52109 52208: gap of 100 bp

52209 52949: contig of 741 bp in length

52950 53049: gap of 100 bp

53050 53777: contig of 728 bp in length

53778 53877: gap of 100 bp

53878 54631: contig of 754 bp in length

54632 54731: gap of 100 bp

54632 54731: gap of 738 bp in length
                                                                                                                                                                                              site:http://genome.wustl.edu/gsc/index.shtml
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50475: contig of 748 bp
50575: gap of 100 bp
51296: contig of 721 bp
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57177: contig of 757
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55569: gap of 100 bp
56320: contig of 751 bp
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03: gap of 100 1
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150210 bases at least Q40
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Pred. No.
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of 751 bp in length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NOTE: This is a 'working draft' sequence. It currently consists of 17 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Caps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
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be preserved.
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                                                                             /note="assembly_name:Contig16"
25799. .32439
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                                                                                                                                                                                                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="15"
        note-"assembly_name:Contig19"
                                  note="assembly_name:Contig18"
                                                             note="assembly_name:Contig17"
                                                                                                                note="assembly_name:Contig15"
                                                                                                                                            note="assembly_name:Contig14"
                                                                                                                                                                                                                            note="assembly_name:Contig11"
                                                                                                                                                                                                                                                                                      /clone="RP11-94P14"
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of 16889 bp in
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                                                                                                                                                                                               Direct Submission
Submitted (01-MAR-2001) DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
On Mar 1, 2001 this sequence version replaced gi:8576139.
Draft Sequence Produced by DOE Joint Genome Institute
WWW.jgi.doe.gov
                                                                                                                           www-shgc.stanford.edu
Quality: Phrap Quality >=40 99.8% of Sequence;
Estimated Total Number of Errors is 0.2.
                                                                                                                                                                          Finishing Completed at Stanford Human Genome Center
                                                                                                                                                                                                                                                                                           Submitted (29-FEB-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA 3 (bases 1 to 170264) DOE Joint Genome Institute and Stanford Human Genome Center.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (20-APR-2000) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Jan 10, 2001 this sequence version replaced gi:7798794. All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Roy,A., Santos,R., Schauer,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Tirrell,A., Travers,M., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         McCarthy,M., McEwan,P., McGurk,A., McKernan,K., McPheeters,R., Meldrim,J., Meneus,L., Mihova,T., Miranda,C., Mlenga,V., Morrow,J., Murphy,T., Naylor,J., Norman,C.H., O'Connor,T., O'Donnell,P., O'Nell,D., Olivar,T.M., Oliver,J., Peterson,K., Pierre,N., Pisani,C., Pollara,V.M., Raymond,C., Riley,R., Rogov,P., Rothman,D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Galagan, J., Gardyna, S., Ginde, S., Goyette, M., Graham, L., Grand-Pierre, N., Grant, G., Hagos, B., Heaford, A., Horton, L., Grand-Pierre, I., Johnson, R., Jones, C., Kann, L., Karatas, A., Klein, J., LaRocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Larocque, K., Lamazares, R., Landers, T., Lehoczky, J., Klein, J., Landers, T., Lehoczky, J., Klein, J., Landers, T., Lehozky, J., Landers, T., Landers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodge,S., Domino,M., Doyle,M., Ferreira,P., FitzHugh,W., Gage,D.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Birren, B., Linton, L.,
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1 (bases 1 to 202915)
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                                                                                                                                                               Sequencing vector: M13; M77815; 49% of reads sequencing vector: Plasmid; n/a; 51% of reads Chemistry: Dye-terminator Big bye; 100% of reads Assembly program: Phrap; version 0.960731 Consensus quality: 199511 bases at least 040 Consensus quality: 201020 bases at least 030 Consensus quality: 201685 bases at least 020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               repeats were identified using RepeatMasker:

A.F.A. & Green, P. (1996-1997)
                                   Quality coverage: 9.5 in Q20 bases; agarose-fp Quality coverage: 9.1 in Q20 b.
                                                                                                                                                                                                                                                                                                                                                                                                                              Center clone name:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center project name: L7430
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: sequence_submissions@genome.wi.mit.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ₩eb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Center code: WIBR
                                                                                                     Insert size: 194000; agarose-fp
Insert size: 202215; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Center: Whitehead Institute/ MIT
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      working draft' sequence. It currently
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AF235106.2 GI:8151913
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WORKING DRAFT SEQUENCE,
Homo sapiens
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5649 7747; contig of 2099 bp in length
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/db_xref="taxon:9606"
/chromosome="4"
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tive 0; Mismatch
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9: gap of 100 bp
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* NOTE: This is a 'working draft' sequence. It currently consists of 9 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown.

* This record will be updated with the finished sequence was soon as it is available and the accession number will
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/clone="GS1-110g02"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                                                                                            70.8%; Score 17; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    808 others
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Karatas, A., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrim, J., Molla, M., Morris, W., Morrow, J., Mychalecky J.J., Naylor, J., Miloff, M., O'Connor T., O'Donnell, P., Pavlin, B., Peterson, K., Pollara, V., Riley, R., Roberts, D., Roy, A., Severy, P., Stange-Thomann, N., Stojanovic, N., Stone, C., Subramanian, A., Tesfaye, S., Torruella-Miller, I., Vassillev, H., Vo, A., Wagner, A., Wheeler, J., Wu, X., Wyman, D., Ye, W.J. and Zody, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (02-MAR-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On Mar 2, 1999 this sequence version replaced g1:4314281.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            All repeats were identified using RepeatMasker:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Donelan,L., Doyle,M., Ferreira,P., FitzHugh,W., Forrest,C., Funke,R., Gage,D., Galagan,J., Gardyna,S., Gilbert,D., Grant,G., Hagos,B., Heaford,A., Horton,L., Howland,J.C., Jones,C., Kann,L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Castle, A., Cerny, J., Colangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Depayre, E., Devon, K., Dewar, K., Donelan, I., Dovle M., Especies, P., Devon, K., Dewar, K., Doven, K., Dewar, K., Dewar, K., Dewar, K., Doven, K., Dewar, K., Dewar, K., Doven, K., Dewar, C., Dewar, M., Dewar, C., 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (25-FEB-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baker, J., Baldwin, J., Barna, N., Beckerly, R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Research, 320 Charles Street, Cambridge, MA 02141,
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AC006924.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P. (1996-1997)
                                                                                /rpt_family="HERV23"
1961. .2607
complement(2544. .2680)
                                                                                                                                                                                                                                        /rpt_family-"MER57B'
466. .519
                                                                                                                                                                                                                                                                                                                complement(220.
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                                                                                                                                                                                            rpt_tamily="LTR24B"
                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RPCI-11 human BAC library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165633 bp
                                                                                                                                                                                                                                                                                                                                            family-"MER57-internal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nusbaum, C. and Lander, E.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-MAR-1999
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20928. .21613
                                                                                          complement(17141. .17494)
/rpt_family="LTR33"
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complement(15533 ..15801)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(4237. .4340)
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_family="MIR"
                                                                                                                                                                _family="(CA)n"
6. .16574
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _family="L1MC5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    _family="L1MC5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 _family-"L2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="AT_rich"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            _family="HAL1"
. .5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   _family="MLT1A2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      _family="MLT1A2"
lement(4)?"
                                                                                                                  family-"Ricksha"
                                                                                                                                                                                                       family-"AluSq"
                                                                                                                                                                                                                                                                                                                                                                          family-"Ricksha"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                _family="AT_rich"
. .7037
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lement(2899..3023)
_family="MSTB"
                                                                                                                                                family-"AluSq"
                                                                                                                                                                                                                                 family-"Ricksha"
                                                                                                                                                                                                                                                                                                                   family-"(TTTC)n"
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                          ACU/9569 239254 bp DNA HTG 02-SEP-2000 Mus musculus clone RP23-71M4, WORKING DRAFT SEQUENCE, 28 unordered pieces. ACU79569
                                                                                                                                                                                              l Similarity 100.
17; Conservative
AC079569.1 GI:9964934
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                   /rpt_fanily="MER65B"

complement(43006. .43358)
/rpt_fanily="MER58B"
43880. .43913
                                                                                                                                                                                                                                                   /rpt_family="AluSx"
complement(46485. .46594)
/rpt_family="MER94"
complement(46595. .46942)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /rpt_family="LTR40a"
complement(38819..39917)
/rpt_family="LIMA8"
                                                                                                                                                                                                                                                                                                                                                                                             /rpt_family="(TATAA)n"
complement(42529, .426
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complement(28398.
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/rpt_family="(TTTG)n"
complement(22880. .23161)
/rpt_family="Alux"
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/rpt_family="Aluy"
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5. .38404
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5. .26237
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Consensus quality: 225489 bases at least Q30
Consensus quality: 225597 bases at least Q30
Estimated insert size: 192000; agarose-fp estimation
Estimated insert size: 236554; sum-of-contigs estimation
Quality coverage: 9.6 in Q20 bases; agarose-fp estimation
Quality coverage: 7.79 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 28 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (02-SEP-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Summary Statistics
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DOE Joint Genome Institute.
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DOE Joint Genome Institute.
Sequencing of Mouse
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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   Consensus quality:
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Center Code: JGI
                                                                        Center Project Name: 1855075
Center clone name: RPCI-23_307N3
                                                                                                                                                                                Direct Submission
Submitted (02-8EP-2000) Production Sequencing Facility, DOB Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
                                                Summary Statistics
                                                                                                     Project Information
                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Rodentia;
1 (bases 1 to 252746)
DOE Joint Genome Institute.
                                                                                                                                 Web site: http://www.jgi.doe.gov
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DOE Joint Genome Institute.
                                                                                                                                                                                                                                                                               Sequencing of Mouse
                                                                                                                                                                                                                                                                                                                                                       Mus musculus
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Mammalla; Eutherla; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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50089 c 50681 g 67592 t 2704 others
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/db_xref="taxon:10090"
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177486: contig of 18691 bp in
177586: gap of unknown length
203950: contig of 26334 bp in
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81831:
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Pred. No.
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Estimated insert size: 206000; agarose-fp estimation Estimated insert size: 249646; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (07-JUN-1996) to the DDBJ/EMBL/GenBank databases. Kiyoyoshi Mishita, Hokkaido University, Department of Chemistry, Faculty of Fisheries; 3-1-1, Minato-Cho, Hakodate, Hokkaido 041-8611, Japan (E-mail:nishita@fish.hokudai.ac.jp, Tel:81-138-40-8800, Fax:81-138-40-8800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei; Acanthomorpha; Paracanthopterygii; Gadiformes; Gadoidei; Gadidae; Teleostei; Metazone
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Theragra chalcogramma
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                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                                             Nishita, K.
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AtvnpykwlpvydQscvnayrgkkrmeapphifsvadnaygfmvtdrenqsclitges
Gagktvntkrvipvfativisgghkaadvgagkikgsledqiiaanplleaygnaktv
Rndnssrfgkfiriffhangkhssadietylleksrvsfqlpdergyhiffqmmtnhk
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TGAVLHHGNMKFKQKQREEQAEPDGNEEADKICYLLSLNSADMLKALCYPRVKVGNEY
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/protein_id="BAA12887.1"
/db_xref="GI:1396064"
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/db_xref="taxon:48550"
/tissue_type="skeletal muscle"
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Score 16; Pred. No.

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DEFINITION

AB017819 3923 bp mRNA VRT 30-SEP-1998
Theragra chalcogramma mRNA for myosin heavy chain, partial cds.

KEYWORDS ACCESSION ERSION

AB017819.1 GI:3668186

AB017819

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8 tattttgggcttcact 23
                                                                  l Similarity
16; Conserv
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Nishita,K., Ojima,T. and Watabe,S.
Direct Submission.
Direct Submission.
Submitted (22-SEP-1998) to the DDBJ/EMBL/GenBank databases.
Klyoyoshi Nishita, Hokkaido University, Department of Chemistry, Paculty of Fisheries; 3-1-1, Minato-Cho, Hakodate, Hokkaido 041-8611, Japan (E-mail:nishita@fish.hokudai.ac.jp, 7el:81-138-40-8800, Fax:81-138-40-8800)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Determination of Primary Structure Walleye Pollack Myosin Heavy Chain Fish Sci. (1998) In press
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ojima, T., Kawashima, N., Inoue, A., Amauchi, A., Togashi, M., Watabe, and Nishita, K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               myosin heavy chain.
Theragra chalcogramma skeletal muscle cDNA to mRNA.
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                                                               Conservative
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ATDAAIDILGETSEDKVAIFKFTGAVLHHGNMKFKQKQREEQAEDDGNEEADKICYLL
SLNSADMLKALCY PRVEVGNEYYTKGOTYPQVNNSYSALAKSIYERLFLAMVIRIUM
LDTKQARQFY IGVLDIAGFEIFDYNSHEQUECHFEKLQOFFNHTMFVLEQEEYKKE
GIIWEFIDFGMDLAACIELIEKRMGIFSILEEECMFFKASDVTFKKLFDDLGENKA
FEKPKPAKDKAEAHFSLVHYAGTVDYNVTGMLDKNKDPLNDSVIGLYQKSSNKLLPVL
YPPVEEVGGAKKGGKKKGGSMOTYSSOFRENLJKLMTHLSTHPHFVRCLIPNESKT
PGLMENHLVHOLECNKOLEGIRICTKGFPSRIIYADFKORYKVLNASVIPDGQEIDN
KKASEKLLGSIDVPHDEYKFGHTKVFFKAGLLGTLEEMDEKLAALVGMIQAAGRGYV
MKKETVKMTERREAVYTIQYNIRSFMNVKHPPMKVYYKTKPLLKSAETEKELANKKE
NYDKMKTDLAAALAKKKELEÖKMYSLLQEKNDLSLQMASDGDNLNDAEERCEGLIKAK
IQLEAAVKETTERLEDEEZINAELTAKKRKLEDECSELKKDIDDLETILAKVEKKHA
TENKVKNLTEBMASODESVAKUTKEKKALQESHQOTLDDLQAEEDKVNTLTKAKTKLE
QOVDDLEGSLEQEKKLANDLERSKRKLEGEKLAALQESTVDLAANGAEKKKELE
GOVDDLEGSLEQEKKLANDLERSKRKLEGEKLAALQESTVDLAAKORGKY
TENKVKNLTEBMASODESVAKUTKEKKALQESHQOTLDDLQAEEDKVNTLTKAKTKLE
GOVDDLEGSLEQEKKLANDLERSKRKLEGEKLAALQESTVDLENDKQQSDEKIKKKDFE
TENKVKNLTEBMASODESVAKUTKEKKALGESHQOTLDDLQAEEDKVNTLTKAKTKLE
                                                                                                                                                                                                                                       LGEQIDNLQRVKQKLEKEKSEYKMEIDDLSSNMEAVSKAKGNLEKICRALEDQLSEIK
AKSDENARQVNDISAQRARLLTENG"
a 854 c 1067 g 851 t
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EISERLEEAGGATSAQIEMNKKREAEFQKLRRDLEESTLQHEATASALRKKQADSVAE
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SLEDQIIAANPLLEAYGNAKTVRNDNSSRFGKFIRIHFHANGKLSSADIETYLLEKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mstdaemaiygaaaiylrkpererleaqstpfdakaaayvadvk
elyvkctmtkadagkytvtvllatkeertvkeddvypmnppkydkiedmamathlneas
vlynlaeryaammiytysglfcatvnpykmlpyydqscvnayrgkkrmbapphipsvs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="myosin heavy chain"
/protein_id="BAA33452.1"
/db_xref="GI:3668187"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /db_xref="taxon:48550"
/tissue_type="skeletal muscle"
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                                                                                        66.7%;
                                                         Score 16; DB Pred. No. 89; 0; Mismatches
                                                            0;
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by cDNA Cloning
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SOURCE
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AE001138/c
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                                                                                                                                                         AE001138
Borrelia
AE001138
                                                                                                                                                                                                                                                                                                                              16;
Fraser, C.M., Casjens, S., Huang, W.M., Sutton, G.G., Clayton, R., Lathlgra, R., White, O., Ketchum, K.A., Dodson, R., Hickey, E.K., Gwinn, M., Dougherty, B., Tomb, J.F., Fleischmann, R.D., Richards
                                                 burgdorferi group.
1 (bases 1 to 11199)
                                                                                            Lyme disease spirochete.
Borrelia burgdorferi
                                                                                                                                           Borrelia burgdorferi (section AE001138 AE000783 AE001138.1 GI:2688210
                                                                            Bacteria; Spirochaetales; Spirochaetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Direct Submission
Submitted (04-SEP-2000) Molecular Cardiovascular Biology,
Submitted (04-SEP-2000) Molecular Cardiovascular Biology,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cincinnati, OH 45229, USA
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Sanbe, A., Gulick, J. and Robbins, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sanbe,A., Gulick,J. and Robbins,J. Ventricular-specific transgenic replacement using
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus ventricular myosin regulatory light chain gene, promoter, exons 1 and 2, and partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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1589 c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="MAPKKAKKRIEGGSSNVFSMFEQTQIQEFKE" 6209. .6298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         join(5446. .5489,6209. >6298)
/product="ventricular myosin r
join(5487. .5489,6209. >6298)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="ventricular myosin regulatory light chain"
/protein_id="AAG40240.1"
/db_xref="GI:11761911"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /number-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/strain="129/J"
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Genomic sequence of a Lyme disease spirochaete, Borrelia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted (12-DEC-1997) The Institute for Genomic Research, 9712
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                                                                                                                                                                                                                                                                                                  /note="similar to PID:1000340 GB:AE000783 percent identity: 34.62; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFVEVVLIDVGRPLFSFPKENFLFLITLGGDGTVLLAVNLLLENENIDIPIISINMGN
VGFLADIKIEDFKKVLDRFFNNSLVINKKFLLHVTVSQHGKDLISKYALNDIIIRSSV
LNKMIYVDLMVNSESFLSYKSDGIIVSTPTGSTGYSFSAGGPTLEADLEGFXLTPISP
complement(1638. .2216)
                          /gene="BB0313"
                                                                           DKCEFDDIPYKDQYEE"
                                                                                   /translation="MFRKESSKDSRSQLQVAGFKIGKESYGVSIEHIREIIKVDSEGVYALPNVPEYIIGIYNLRGSIIPLINLNIKFGVPSISVTEEDMLLTGYLIVKIKNKLLG
IFVDRVLKVISFDDSRVQEFPATLQFLDRKYISGVVKLDEADNLESEYLVLIDIAKIF
                                                                                                                                                                         /product="purine-binding chemotaxis protein (cheW-1)"
/protein_id="AAC66698.1"
/db_xref="GI:2688217"
                                                                                                                                                                                                                                                                                                                                                                           complement(1064. .1594)
/gene="BB0312"
                                                                                                                                                                                                                                                                                                                                                                                                                             complement(1064. .1594)
/gene="BB0312"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       complement(235..1116)
/gene="BB0311"
complement(235..1116)
/gene="BB0311"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VSFCTDTFVKRLKNKLL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="conserved hypothetical protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="similar to GB:L42023 SP:P44497 PID:1003048 PID:1221979 PID:1204329 percent identity: 33.49; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="MFFLIKIFLGCCLNVWFNLIFNKVRGFYMFYYKDFNVLFIRRVN
V"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /db_xref="taxon:139"
complement(77..214)
/gene="BB0310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HSVYNRSFVFSKLSKLSISFSKEYFIAAASIFLDGINFGSFGVDVVFEFKISSQSLNF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="BB0310"
                                                                                                                                                                                                                                                   /transl_table=11
                                                                                                                                                                                                                                                                               /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /translation="MINANLTTFPIKINMKNKVLLCINTLKSGASILGNDVKVYLETK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identified by sequence
/codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="B. burgdorferi
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/db_xref="GI:2688224"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            putative"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="hypothetical protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ∕organism="Borrelia burgdorferi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      predicted coding region BB0310"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         identified by Glimmer;
                                                                                                                                                               gene
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identity: putative"
                                                                                              complement(4805. .5737)
                                                                                                                              /gene="BB0317"
                                                                                                                                                                                FPISFLIVFFEYQFFRTQEYVNSYFSLSFQFYVAIIINILVSLIKRKDRS*
                                                                                                                                                                                                         /translation="MfSIFEQAIVESYLALGYLYTEKIGFLNYSIEGISYLSIFLTSF
FIYLGYGIFMSTIFTLFISFLFGFFLSFVVKKNYDIFIAGIGINIFCYFFYXYLMKSN
FNFIPGFTLMLSGNFEIFVFIAVFFIFLFITVYVISYSRIRAVFEFISSGSYEDILGE
KISSRFKSFAIFVSIFTASLAGSFIAVSLNAYSYNLGLNNGWLAICILYIAFSNPLLI
/note="similar to GP:1934813 percent identity: 22.14;
identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MLLKDSKKYNKAIESLTKIINMDQNQADAHLLLSELEYLNKNWKKAIIKSQDYLKIID
FKDKKNFLDISWAYFLIGEVKNSMDYIIKFFQSGKELFRENIFIAIDALFKKSIYHFT
                                                                     /gene="BB0317"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(3998. .4804)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="hypothetical protein; identified by Glimmer;
putative"
                                                                                                                                                                                                                                                                                                                                           /protein_id="AAC66695.1"
/db_xref="GI:2688214"
                                                                                                                                                                                                                                                                                                                                                                                                                             /product="conserved hypothetical integral membrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="similar to GB:L43967
identity: 26.67; identified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="BB0316"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="B. burgdorferi predicted coding region BB0315"
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/db_xref="GI:2688223"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FNQIKNTKTTKARKEIFKLTEMINSSKSIKNSTIVALKYLNEFKNELNLYPLTNRYKN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="octaprenyl-diphosphate synthase (ispB)"
/protein_id="AAC6696.1"
/protein_id="AAC6696.1"
/db_xref="G1:268215"
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YIKAPAIBIVNRGGKRIRPHIMILLAYALGLKEKNTKLIYKLSLLLELPHSGSLIIDD
YIKAPAIBIVNRGASAIHLIYGIDNSINAGNLIYFLPAKLIEKSNLKENOKLLIYENFFTT
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/note="similar to SP:P19641 GB:X68873 PID:388220
PID:606125 GB:U00096 percent identity: 33.65; ide
by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /translation="MRKITIMILFYGLIINVCPTTTTSILKLNKKANKHTIEKLYQKS
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/transl_table=11
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YSTFLKLGVYFQIIDDIKNIKNKINGKEFGDDLLEGKKSLPIIYFLQEKKFEPKIISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="BB0314"
2267. .3310
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Aspgsfsqpaykklkrgilvspuindiglryddnfybikgdiflddyvkinfekpys
Lvisdvapkttgurludtsnsfnlsmriddlsfulkkgnllykvfqggdemqifkk
FEXYFKFYKKIRPKAVRKNSFBIYFLGKSFGK"
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34.36; identified
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/protein_id="AAC66697.1"
/db_xref="GI:2688216"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="BB0313"
/note="similar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PID:1045801 SP:P47367 percent by sequence similarity;
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REFERENCE
AUTHORS
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SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ACCESSION
VERSION
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AC017994/c
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Submitted (09-DEC-1999) Celera Genomics, 45 West Gude Drive, Rockville, MD, USA
This sequence was identified as CDM:10212930 by the submitter. For more information on this record e-mail to fly@celera.com.
* NOTE: This is a 'working draft' sequence.
* This sequence will be replaced
                                                                                                                                                                                                                                                                        Drosophila melanogaster
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 23091)
Adams, M. and Venter, J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AC017994.1 GI:6553196
HTG; HTGS_PHASE2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AC017994
                                                                                                                                                                                                                                                            Direct Submission
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/protein (mglA)"
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/db_xref="Gi=2688212"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product="exported protein (tpn38b)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:U12861 PID:551522 percent identity:
26.33; identified by sequence similarity; putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(7194. .8246)
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LLLLSDNILAMKMGEVLLNVSREKISKEKLKELLFL"
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PID:1220920 PID:1205071 percent identity: 32.53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NFLNINYDFKYEFIGLCQSIAIFISLFLIKARKK" complement(5734. .7194)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ^translation="MIFFRNSFMALIFSESILSISYFFGDFFOFSYIKMISWRFILFL
IMATGIATCAKSNSIMLGNESQIYFGAFUNYIFSSFFGTIYYFMYFFLILLSSFFYGLL
GLIPPFITFFFGLHKALTGLLISYGMORLUDGILMNLKTGSFSNQTKRINSLFALDS
SLIYLFLLGVSVWLFYVFIHKKTIYGLQLEILSNKKKIDIFFNINEFKYKFFAVFGSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /codon_start=1
/transl_table=11
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*** SEQUENCING IN PROGRESS ***, in ordered
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1. .23091
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/db_xref="taxon:7227"
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                                                                    66.7%; Score 16; 100.0%; Pred. No.
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                                                                    DB 65; Length 23091; 82;
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Search completed: November 15, 2001, 06:17:26 Job time: 8011 sec

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; TOPOLOGY: 11:
; MOLECULE TYPE:
; HYPOTHETICAL:
US-08-629-939-5
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Patent No. 5645925
GENERAL INFORMATION:
APPLICANT: Kieback,
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-08-629-939-5,
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                                                                                                                                                                                                                                                                               TELEFAX: (202) 293-7860 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                  FILING DATE: 12-ARIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIT, GORDON
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-66
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
LENGTH: 320 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 20037

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                     TELEPHONE: (202)
                                                                                                                                                                                             STRANDEDNESS: single
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COUNTRY: U.S.A.
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5, Application
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US-09-033-333-2
US-09-058-389A-5
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US-09-08-816-010-1
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US-09-033-333-3
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Avenue, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FOR DIAGNOSING AN BREAST OR OVARIAN
                                  Score 18; DB 1;
Pred. No. 0.11;
Mismatches
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SUMMARIES

Total number of hits satisfying

chosen parameters:

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Word size Searched: Title: Perfect score:

US-09-663-020-8 18

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OM nucleic - nucleic search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen

November 15,

2001, 05:55:52;

Search time 49.19 Seconds (without alignments) 82.875 Million cell updates/sec

Scoring table: Sequence:

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US-09-018-5847-6
US-09-385-982-354
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US-09-687-31-7
US-08-696-731-7
US-08-694-915-5 Sequence 5, Appli Sequence 6, Appli Sequence 20, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli Sequence 23, Appli Sequence 12, Appli Sequence 13, Appli Sequence 23, Appli Sequence 23, Appli Sequence 23, Appli Sequence 24, Appli Sequence 1, Appli Sequence 1, Appli Sequence 27, Appli Sequence 7, Appli Description Sequence Sequence

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RESULT 3
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                                                                                                                                                                                                                                                        Sequence 6, Application US/09018584A Patent No. 6238863
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (202) 293-7860 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/.
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
COMPUTER READABLE FORM:
                                                                                                                                 APPLICANT: Bacher, Jeffery W.
TITLE OF INVENTION: IDENTIFYI
TITLE OF INVENTION: REPEAT DN
TITLE OF INVENTION: REPEAT DN
NUMBER OF SEQUENCES: 147
                                                                                                                   CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: A-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                COUNTRY: U.S.A. ZIP: 53711-5399
                                                                                                                                                                                                                                                                                                                                                            96 GGCGGAGCTTGCAGTGAG 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOPTWARE: Patentin Release #1.0, Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 2100 Pennsyr. CITY: Washington, D.C.
                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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REGISTRATION NUMBER: 30,764
                                                                                                                                                                                                                                                                                                                                                                             1 ggcggagcttgcagtgag 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                  Madison
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                                                  Wisconsin
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                                                                                2800 Woods Hollow Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3: SUGHRUE, MION, ZINN, MACPEAK & SEAS 2100 Pennsylvania Avenue, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                       Schumm, James W.
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                                                                                                 Promega Corporation
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                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                 IDENTIFYING AND ANALYZING INTERMEDIATE TANDEM REPEAT DNA MARKERS
                                                                                                                                                                                     MATERIALS AND METHODS FOR
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Pred. No. 0.11;
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     Matches
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                   SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: ENDEGE, WILSON O., ET AL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 354, Application US/09385982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/385,982
CURRENT FILING DATE: 1999-08-30
                                                                                                                                                                                                                                              SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 60/117,393
EARLIER FILING DATE: 1999-01-27
EARLIER APPLICATION NUMBER: 60/098,639
EARLIER FILING DATE: 1998-08-31
                                                                                                                                                                                                                                                                                                                                                   EARLIER APPLICATION NUMBER: 09/328,111 EARLIER FILING DATE: 1999-06-08
                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: NOVEL HUMAN GENES AND GENE EXPRESSION TITLE OF INVENTION: PRODUCTS: II FILE REFERENCE: CCDNA-260XX
                                                                                                                                                                                                                                                               NUMBER OF SEQ ID NOS: 544
                                                                                                    NAME/KEY: misc_feature
LOCATION: (1)...(631)
OTHER INFORMATION: n =
                                                                                                                                                          LENGTH: 631
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (608) 257-2275 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IMMEDIATE SOURCE:
LIBRARY: plasmid,
CLONE: C390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Grady J. Frenchick
REGISTRATION NUMBER: 29,018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: Ci
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       154 GGCGGAGCTTGCAGTGAG 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
SOFTWARE: Word 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 ggcggagcttgcagtgag 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/0 FILING DATE: 04-Feb-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS: Double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6262334
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(608) 257-2275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SYSTEM: Windows 95
Word 97 (DOS text format)
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IBM compatible PC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genomic DNA
                    100.0%; Score 18; DB 4; Length 631; 100.0%; Pred. No. 0.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 18; DB 4; Length 471; 100.0%; Pred. No. 0.1;
                                                                                                       A, T, C or
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RESULT 6
US-08-943-731-171
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Best Local Similarity
"~+~hes 18; Conserve
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; LOCATION:
US-08-755-587-20
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Sequence 171, Application US/08943731 Patent No. 6265157
                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: GB 90 FILING DATE: 28-AUG-1996 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 25-NOV-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 774 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                    REGISTRATION NO.... 54
REFERENCE/DOCKET NUMBER: 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Kenneth D Sibley REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: GB 9: FILING DATE: 14-DEC-1995
                                                                                                                                                                                                                                                                                      LOCATION:
                                                                                                                                                                                                                                                                                                    NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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o. 6045997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION:
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310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
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                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                  CDS
168..274
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                                                                                                                                                                                                                                         166..274
                                                                                                                                                                                                                                                                                                                                                linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UMBER: GB 9617961.9
28-AUG-1996
                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                            double
                                                                                                                                                             100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Materials and methods relating to the identification and sequencing of the BRCA2 cancer susceptibility gene and uses thereof.
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                                                                                                                                                 0;
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                                                                                                                                                            Score 18; DB 3;
Pred. No. 0.099;
                                                                                                                                                Mismatches
                                                                                                                                                                          DB 3; Length 774;
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RESULT 7
US-08-755-587-21/c
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Sequence 21, Application US/08755587 Patent No. 6045997
                                                                                                                                                                    Matches
                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                            TELEFAX: 215-567-2991
TELEX: 831-494
INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: PANITCH SCHWARZE JACOBS & NADEL, P.C.
STREET: ONE COMMERCE SQUARE, 2005 MARKET STREET, 22ND
STREET: FLR.
                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
LENGTH: 863 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 215-965-1284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US 0: FILING DATE: 03-DEC-1991 ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: 1
FILING DATE: 14-MAR-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
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TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING
TITLE OF INVENTION: ALTERED TYPE I OR TYPE IX COLLAGEN GENE SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/943,731 FILING DATE: 03-OCT-1997 CLASSIFICATION: '435
                                                                                                                                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: DOYLE LEARY Ph.D. REGISTRATION NUMBER: 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 19103-7086
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                                                                                                                                                                                                                                                                                                                 nucleic acid
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                                                                                                                                                                 Conservative
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SPOTILA, LORETTA D.
DELTAS, CONSTANTINOS D.
SEREDA, LARISA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLIGE, ALAIN
EARLY, JAMES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PACK, MICHAEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                                                                100.0%;
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                                                                                                                                                                             Score 18; DB 4; Length 863; Pred. No. 0.098;
                                                                                                                                                                 Mismatches
                                                                                                                                                               Indels:
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GENERAL INFORMATION: APPLICANT: Futrea

Wooster, Richard

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APPLICANT:

Ashworth,

Michael R

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US-08-755-587-21
                                                                                                                                                                                                 Sequence 3, Applic Patent No. 5968735
                                                                                                                                                                                                                                                                                                                                                         Matches
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                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER: 5
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
                                                                                                             APPLICANT: STEIN, Ulrike
APPLICANT: WALTHER, Wolfgang
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                       NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Kenneth D Sibley
NAME: State Brand NUMBER: 31,665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 14-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 90
FILING DATE: 28-AUG-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: GB 9523959.6
FILING DATE: 23-NOV-1995
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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COUNTRY:
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                                      ADDRESSEE: NIKAIDO, MARMELSTEIN, STREET: 655 Fifteenth Street, N. STREET: Street Lobby
                                                                                                                                                                                                                                                                                               29
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nes 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/755,587 FILING DATE: 25-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY:
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                           Washington
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USA
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310 UCB Plaza, 3605 Glenwood Avenue, PO Drawer 31107
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501..550
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                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                      W., Suite 330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                  0;
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US-08-439-814-2:
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                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: STEIN, Ulrike
COUNTRY: USA
ZIP: 20005-5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                    APPLICANT: STEIN, ULLIANG APPLICANT: STEIN, WOLFGANG APPLICANT: WALTHER, WOLFGANG FOR THE EXPRESSION OF THE TAVENTION: THERAPY-RELEVANT GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRANDEDNESS:
TOPOLOGY: line
MOLECULE TYPE: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 3
                                                                                                                                             CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: DE P
FILING DATE: 10-NOV-1993
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: DE P 4238778.7 FILING DATE: 12-NOV-1992 PRIOR APPLICATION DATA:
                                                                      CITY:
STATE:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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                                                                                                  STREET:
                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.30B (EPO)
                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: DE PA
FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                        1 ggcggagcttgcagtgag 18
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TELEFAX: 202/638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 36,335
REFERENCE/DOCKET NUMBER: P1614-5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ENGTH:
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                                                                                                                                                                                                                                                                                                                                                       GGCGGAGCTTGCAGTGAG 22
                                                                  Washington
DC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             nucleic acid
DEDNESS: single
                                                                                                                                                                                                                                                                         Application US/08439814
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                                                                                                  655 Fifteenth Street, N. Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linear
                                                                                                         NIRAIDO, MARMELSTEIN, MURRAY & ORAM LLP
5 Fifteenth Street, N. W., Suite 330 G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA (genomic)
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Pred. No. 0.094;
                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: DE P42
FILING DATE: 12-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT
FILING DATE: 10-NOV-1993
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                     atent No.
                                                                                                                                                                                   APPLICANT: Belt, Judith A.
APPLICANT: Crawford, Charl.
APPLICANT: Patel, Divyen
TITLE OF INVENTION: A NITR
TITLE OF INVENTION: PROTEI
TITLE OF INVENTION: USE
                                                                                                                                                                                                                                                                                                                   SENERAL INFORMATION:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 1688 base pair:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30B (EPO)
PRIOR APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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APPLICATION NUMBER:
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                                                                                                        STREET: 411 H
                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: 202/638-500
TELEFAX: 202/638-4810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: KLESNER, Sharon N. REGISTRATION NUMBER: 36,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: DE P
FILING DATE: 12-NOV-1992
                                                                                                                                          ADDRESSEE:
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REFERENCE/DOCKET NUMBER: P1614-5015
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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No. 6130065
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                                         07601
                                                                                         Hackensack
                                                                      New Jersey
                                                                                                                                                                                                                                                                                                                                                   Application US/09058389A

    David A. Jackson, Esq.
    Hackensack Ave, Continental Plaza, 4th

                                                                                                                                                                                                                                                                             Crawford, Charles R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                       USA
                                                                                                                                     David A. Jackson,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA (genomic)
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                                                                                                                                                                                                                                                                                                 Judith A.
                                                                                                                                                                                                       A NITROBENZYLMERCAPTOPURINERIBOSIDE (NBMPR)-INSENSITIVE, EQUILIBRATIVE, PROTEIN, NUCLEIC ACIDS ENCODING THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 18; DB 2; Length 1688; Pred. No. 0.092;
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SAME AND METHODS OF
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RESULT 11
US-08-439-814-1
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Best Local Similarity
Watches 18; Conserva
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; HYPOTHETICAL:
US-09-058-389A-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 1,
                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                        FILING DATE: 12-MAY-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/439,814
                                                                                                                                                                                                                                                                                                                                      APPLICANT: STEIN, WALTHER, WOLIGANG
APPLICANT: WALTHER, WOLIGANG
TITLE OF INVENTION: VECTOR FOR THE EXPRESSION OF
TITLE OF INVENTION: THERAPY-RELEVANT GENES
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
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                              APPLICATION NUMBER: DE P
FILING DATE: 12-NOV-1992
                                                                                                                                                       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                         COMPUTER:
                                                                                                                                                                                                                    COUNTRY: USA
ZIP: 20005-5701
                                                                                                                                                                                                                                                       STATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 ggcggagcttgcagtgag 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                  Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
DEDNESS: double
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                                                                                                                                                                                                                                                                                 EE: NIKAIDO, MARMELSTEIN, MURRAY & ORAM LLP
655 Fifteenth Street, N. W., Suite 330 G
Street Lobby
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1712 base pairs
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                                                                                           12-MAY-1995
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/desc = "intron 2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                             DE P 4238778.7
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Pred. No. 0.091;
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FILING DATE: 10-NOV-1993 ATTORNEY/AGENT INFORMATION:

DE PCT/DE93/01086

REGISTRATION NUMBER:

OCKET NUMBER

36,335

P1614-5015

INFORMATION:

KLESNER, Sharon

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Patent No. 608408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: WO PCT/DE93/01086 FILING DATE: 10-NOV-1993 INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/609,583
FILING DATE: 01-MAR-1996
APPLICATION NUMBER: US 08/487,748
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                      ATTORNEY/AGENT INFORMATION:
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APPLICATION NUMBER: DE P4238778.7
FILING DATE: 12-NOV-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 3
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                                   TELEFAX:
                                                                                    REFERENCE/DOCKET NUMBER:
                                                                                                    REGISTRATION NUMBER:
                                                                                                                                                        FILING DATE: 03-MAR-1995
                                                                                                                                                                     FILING DATE: 07-JUI
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                             CLASSIFICATION: 536
                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/829,525
FILING DATE: 28-MAR-1997
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                                                                                                                                                                                                                                                                                                                                                                               COMPUTER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: PatentIn Release #1.0, Version #1.30B (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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TELEPAX: 202/638-4810
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                                                                                                                  Coruzzi, Laura A.
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COMPOSITIONS AND METHODS FOR
TREATMENT AND DIAGNOSIS OF IM
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US-08-609-583A-23/c
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Best Local Similarity
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                                                                                                                                      NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS LENGTH: 2236 base pair
                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
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COMPUTER READABLE FORM:
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                                                                EATURE:
                                                                             OLECULE TYPE:
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LENGTH: 2236 base pairs
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                OTHER INFORMATION:
                                                                                                                                                                                     TELEPHONE: Z12 TELEPHONE: Z12 869-8864
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APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995
                                                                                            TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/487,748 FILING DATE: 07-JUN-1995
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                                                                                                                        TYPE: nucleic acid
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                                                                                                                                                                                                                                                                  NAME: Coruzzi, Laura
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ Version 2.0
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LOCATION: 42...944
OTHER INFORMATION: Human 200 gene nucleotide
OTHER INFORMATION: sequence
                              LOCATION:
                                               NAME/KEY:
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1155 Avenue of the Americas
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                                                                                                                                                                                                                                                                                Laura A
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sequence
         Human 200 gene nucleotide
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US-08-609-583A-23

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Query Match
Best Local Similarity
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                             Mismatches
                                     0.089;
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OTHER INFORMATION:
OTHER INFORMATION:
US-08-937-399-23
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
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                                                                                                                     NAME/KEY:
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                                                                                                                                                                                 STRANDEDNESS:
TOPOLOGY: 111
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APPLICATION NUMBER: US 08/398,633
FILING DATE: 03-MAR-1995
                                                                                                                                                                                                        LENGTH: 2236 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                     NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/609,583 FILING DATE: 01-MAR-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/937,399
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COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF IMMUNE DISORDERS
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Pred. No.
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0.089;
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                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
APPLICATION:
FILING DATE: 26-FEB-100
ATTORNEY/AGENT INFORMATION:
NAME: Meiklejohn, Ph.D., Anita L.
NAME: Meiklejohn, Ph.D., Anita L.
ATTORNEY/AGENT ANIMBER: 35,283
                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 07
TELECOMMUNICATION INFORMATION: 617/542-5070
                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
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                                                                                                                                                           FEATURE:
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APPLICANT:
                                                                                                                                                                   MOLECULE TYPE:
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TELEFAX: 200154
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OPERATING SYSTEM:
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225 Franklin Street.
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linear
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